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Database :
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1: gb_ba:*
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ALIGNMENTS

REFERENCE	ORGANISM	SOURCE	VERSION	ACCESS TO A PARTY OF	LOCUS	RESULT 1 AP004676/c
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.	Crysa sativos_Boo. Oryza sativo (japonica cultivar-group) Eukarvota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:	Oryza, Alios_PHASE2. Oryza, Sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,	AP004676. 1 GI:18447935	OJIO03_806, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	AP004676 131955 bp DNA linear HTG 21-MAR-2002	

Pred. No.

is the number of results predicted by chance to have a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agrobiological Sciences, Rice Genome Research Program; Kannondai 2:1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, uRL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by combining Monsanto and RCP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGCTCCCAGCTCACCTGTCATCGCCTCCACTCACTAAAATGCCGCCGCGCGCTGGGTCCAT 146
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GCGCATCTTCCGCGAACTCCGTGGCCACCGGTGAGGTCTACCCGTTGGAGCTAGCGGA
                               GCGCATCTTTTTCGCAACTCCGTGGCCACTGGAGAGGTGTACCCCTCTGGAGCTCACGGA 557
                                                                      GCACGCGCCCGTCGCGCTTGGGGGCCCGCTGCGCCATTGTTGCCSGAGGGCTACGC 497
                                                                                                                                          GACCACCCGCTACGCCGTCATCATCGGCGGCGCCAACTTCGGCTGCGGCTCCTCCCGCGA 87178
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Direct Submission
Submitted (30-JAN-2002) Takuji Sasaki, National Institute of
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/chromosome="2"
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/cultivar="Nipponbare"
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Pred. No. 5.4e-85;
1; Mismatches 149;
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                                                                                                                                                                                                                                                                                   Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nlas.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, rel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of locatigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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/db_xref="taxon:39947"
/chromosome="2"
/clone="P0519E06"
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78.28;
                                        Score 462.2; DB 2;
Pred. No. 5.7e-85;
1; Mismatches 149;
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lipase-like protein; plastid ribosomal protein L19; PREG-like protein; uclacyanin 3-like protein; vesicle-associated membrane protein; w1050ERIFDK gene; W1110ERIFDM gene; W1205ERIFDK gene; protein; W1050ERIFDM gene; W1105ERIFDK gene; W1245ERIFDK gene; W230ERIFDM gene; W265ERIFDK gene; W30ERIFDM gene; W325ERIFDM gene; W380ERIFDM gene; W420ERIFDM gene; W435ERIFDM gene;	gene; C800ERIEDM gene; C805ERIEDM gene; C90ERIEDM gene; daad-like protein; enoyl-CoA hydratase; ethylene responsive element binding; fibroin; glycerol 3-phosphate permease; GTP-binding protein;	gene; C180ERIPDM gene; C200ERIPDK gene; C202ERIPDK gene; C285ERIPDM gene; C395ERIPDM gene; C395ERIPDM gene; C395ERIPDM gene; C395ERIPDM gene; C440ERIPDK gene; C555ERIPDM gene; C600ERIPDM gene; C650ERIPDM gene; C740ERIPDM gene; C740ERIPDM gene; C785ERIPDM gene;	gene; C175ERIPDM gene; C1275ERIPDM gene; C135ERIPDM gene; C1265ERIPDM gene; C1275ERIPDM gene; C1265ERIPDM gene; C1275ERIPDM gene; C1265ERIPDM gene; C1275ERIPDM gene; C1265ERIPDM	subunit 8-like; AP2-related transcription factor; aquaporin; configuration factor; AP2-related transcription factor; aquaporin; configuration factor; AP2-related transcription factor; aquaporin;	ACCESSION AJ307662 FULL ACCESSION AJ307662. GI:14140112	339972 bp DNA lin			1	678 CCCTGTAATTGAGGCGGGAGGGATCTTTGCCTACGCCCGGAAGACAGGAATGATTGCGTC	VY 010 CHITITHATCHCHCCTCTGGCARGGAGTGCAAGCTGAAGCTGATGGTGATGCTGG 6// LI	29528 CACTGGAGCCTGGAAGGAGTGCAAGACCGGGGATGTGGTCACGGTGGAACTTGATAATTG		29588 GCGCATCTTCTTCCGCAACTCCGTGGCCACCGGTGAGGTCTACCCGTTGGAGCTAGCGGA	498 GCGCATCTTTTTCGCAACTCCGTGGCCACTGGAGAGGTGTACCCTCTGGAGCTCACGGA	OY 438 GCACGCGCCCGTCGCCCTTGGGGCCCCCTGGCGCCATTGTTGCSGAGGGCTACGC 497	29708 GACCACCCGCTACGCCGTCATCATCGGCGCGCCCAACTTCGGCTGCGGCTCCTCCCGCGA	Db 29768 CGCCTTCGTCGGCCTCCCCACCGGGGCCTACCCGACGCCGTTCGTCGTCGCCCCGGCGAGGA 29709 Ov 378 GTCCTCCCTACCGTACCCCATCATTCTCGGGCCCGACGACGCAACCTTCGGCGTCGCCTTCCTCTCCCCA /37	318	QY 258 CGCCGAGCACCTCACTCTGGTGCCCTCCAAGCCGGAGGAGGAACCTCGGGTTCCTT 317	OY 198 CGTTTTCCACGGCGAGTGCTTCGTGGTGGCGACAATATCGACACCGACCAGATCATCCC 257	29948 GACCGCCGTGGTCGCCGCCGCGCTGCGGCTGCGGCGGGGGGACTCGACGTCGGCCGG		OY 87 GCGCTCCCAGCTCATCGTCATCGCCTCACTCAACAATGCCGCCGCGCGGGTCCAT 146 Db 30008 CCGCAGCTGGGTCGCGGCTATCTGCCGGCCCCCTGAAATGCCACCACAGTCGTCCCCT 29949
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                                                                                                                                                                                                                                  CGCCTTCGCGGGGGCTCCCATCCGCGGGCCTACCCGACGCCGTTCGTCGCTCCGGGTGAGGA 377
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                                                                                                                                                                                                                   The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K., Banh,J., Banno,F., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheu,H.R., Jones,T. Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C. Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.
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2 (bases 1 to 787)

Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Cheuk, R., Hayashizaki, Y., Kim, C., Koesema, E., Lam, B., Lin, J., Karlin Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-NOV-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA. The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CMA'): Scki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                     Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis Open Reading Frame (ORF) Clones Unpublished
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="2"
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                                   TCGAAAGCTGCTGCAT 751
                                                                                              GGCCCTGTAATTGAGGCGGGAGGGATCTTTGCCTACGCCCGGAAGACAGGAATGATTGCG
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KPLVSKASSSFVTRSAAEPQEKKTFHGJCYVYGDNIDTDQIIDAEFLTLVPSNPEEY
KPLVSKALVGLPASYKERFVQPEEMKTRYSJIIGGENFGCGSSREHAPVCLGAAGAKA
VVAQSYARIFFRNSVATGEVYPLDSEVRVCDECTTGDVATVELREGDSILINHTTGKE
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/product="putative 3-isopropylmalate dehydratase,
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AY035158 970 bp mRNA linear PLN 24-Al Arabidopsis thaliana putative 3-isopropylmalate dehydratase, subunit (At2g43090) mRNA, complete cds.

PLN 24-APR-2002

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Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L. (Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Full Length cDNA Clones

2 (bases 1 to 970)
Yamada W. Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopl
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopl
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koseema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-MAY-2001) Plant Gene Expression Center, 800 Buchan, Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFI cDNAs (RAFL cDNA: 'KIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AY035158
AY035158.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., O Quach,H.L., Tang,C.C., Toriumi,M., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SC contributed equally to this work as PIS.
                                                                                                                                                                                                                                                                                                                                              /clone="RAFL04-10-X01 (R09710)"
/note="This clone is in a modified
/Lambda ZAP) as a XhoI/SstI insert.
ecotype: Columbia"
                                                                                                                                                                                                                                               /gene="At2g43090"
31. .786
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KPLVSREASSSFVTRSAAEPQERKTFHGLCYVVGDNIOTDQIIPAEFLTILVPSNPEEY
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VVAQSYARIFFRNSVATGEVYPLDSEVRVCDECTTGDVATVELREGDSILLNHTTGKE
                                                                                                                                                        /evidence=experimental
/product="putative 3-isopropylmalate dehydratase,
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis
/db_xref="taxon:3702"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                 /gene="At2g43090"
/codon_start=1
                                                                                                                                                                                                                                                                                                     /gene="At2g43090"
                                                                                             /protein_id="AAK59662.1"
/db_xref="GI:14334970"
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                                                                                                                                                                                                                                                                       sequence.
AC006224
AC006224.4
Unpublished 2 (bases 1
                                  Benito, M.-I., Carrera, A.J
Nierman, W.C., Fraser, C.M.
                                                            Lin,X., Kaul,S., Shea,T.P.,
Barnstead,M.E., Mason,T.M.,
Benito,M.-I., Carrera,A.J.,
                                                                                                                                                                                                                                                     HTG.
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                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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/gene="At2g43090"
954
                                                                                                               II; Brassicales; Brassicaceae;
Bowman,C.L., Ronning,C.M.,
Creasy,T.H., Buell,C.R., Town,C.D.,
nd Venter,J.C.
                                                                  Fujii, C.Y., Shen, M.,
                                                                                                                                                                                                                                                                                                                         clone MFL8
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                                                                       VanAken, S.E.,
                                                                                                                  Arabidopsis.
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                                                                                                                                                                                           TTAGTTGGTCTTCCA----GCTTCTTACAAGGAACGATTCGTTCAGCCAGGTGAGATGAAG
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AGTATTTGATCATCATACGACTGGGAAAGAGTACAAGCTTAAGCCGATTGGTGATGCT 9082
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                                                                       GGGGCCTGGAAGGAGTGCAAGACAGGGGATGTGGTCACCGTGGACCTTGCTAACTCCG--
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                                                                                                             ATCTTTTTCGCAACTCCGTGGCCACTGGAGAGGTGTACCCTCTGGAGCTCACGGACGTT
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                        TTTTTATTAACCACACCTCTGGCAAGGAGTACAAGCTGAAACCAATTGGTGATGCT 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(<18779. .>19472)
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14957. .1511,15327. .15506,15608. .15642,15728. .15884,
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17197. .17217,17377. .17486)
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Pred. No. 5e-33;
); Mismatches 182;
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 90283)

1 (change 1 to 90283)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-MAR-2000) The In-
Medical Center Dr., Rockville,
3 (bases 1 to 90283)
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TRLDGHTALSIRGNCAFTEKAKHAEAAGASALLVINDKEDLDEMGCMEKDTSLNVSIPV
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ASRYSFSTILSSNPLPRLILAPLFDLRYDKIKKRVISNGYFLWLTIGYGIGLLLTYLG
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Fraser,C.M., Somerville,C.R. and Venter,J.
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VVAQSYARIFFRNSVATGEYYPLDSEVRVCDECTTGDVATVELREGDSILINHTTGKE
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/note="F14B2.3; supported by full length cDNA:
Ceres:31507"
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BNGBLIQYLRYBPQGFYKPHBDY FADTFULKRGGORVATMLAYLTDDYBGGEKTYPPLA
GDGDCTCGGK IMKGISYKPTKGDAYLFWSMGLDGQSDPRSIHGGCEYLSGEKWSATKW
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Local
                                                                                                                      Similarity
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complement(18011. .18045)

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complement(join(<18719. .19272,19634. .>19970))

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complement(29414. .29451)
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LDLAVEHIKGLQHQVEVRP"
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                                                                                                                    20.4%;
                                                                                            Score 210.8; DB 8; Pred. No. 5.8e-33; 0; Mismatches 182;
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available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                   Unpublished
3 (bases 1
                                                                                                                                                                                                                                                                       Genome Biol. (2002) In press 2 (bases 1 to 945)
Broyer, V., Troukhan, M., Alexi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana clone AY087084
                                                                                        Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs
                                                                                                                        Direct Submission
Submitted (11-MAR-2002) Ceres, Inc,
                                                                                                                                                                                  Brover, V., Troukhan, M.,
                                                                                                                                                                                                                                                        Feldmann, K.
                                                                                                                                                                                                                                                                                                                               annotation
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                                                                    GGACCAGTGATTGATGCTGGTGGTATATTTGCTTATGCTAGGAAAGCTGGAATGATTCCA
                                                                                                        GGCCCTGTAATTGAGGCGGGAGGGATCTTTGCCTACGCCCGGAAGACAGGAATGATTGCG
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Genset carried out the library production and sequencing of th
full-length clones. Ceres, Inc. carried out the clustering of
5' sequences, selection of clones, and sequence assembly.
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208 c 210 g 281 t
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/protein_id="AAM64645.1"
/db_xref="GI:21592696"
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/db_xref="taxon:3702"
/clone="31507"
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2 (bases 1 to 802)
2 (bases 1 to 802)
Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Panda, K., Banh, J., Chan, M., W., H.C., Yamamura, Y., Yu.G., Bowser, L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu.G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Kim, C., Lam, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Salk, Stanford, PGEC (SSP) Consortium members constructed an sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K., Banh,J., Chan,M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Palan,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (03-JUN-2002) plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94/10, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contributed equally to Location/Qualifiers
                                                                                                                                                                                                                                                                /gene="At2g43100"
1. .771
                                                                                                                                                                                                                                                                                                                                                             /note="This clone ecotype: Columbia"
/protein_id="AAM51283.1"
/db_xref="GI:21436289"
/translation="MAYSLPTFPQALPCSSTKTSSSLATFRSPFLRFNGSTSLIPSSI
                                                                                                                            /evidence=experimental /product="putative 3-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equals. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP ntributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis
/db_xref="taxon:3702"
                                                                                                                                                                                              /gene="At2g43100"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="U11883"
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complete cds.
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ACCESSION
VERSION
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ORIGIN
                                                                 REFERENCE
                                                                                                                                                                     KEYWORDS
                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 CATCGTCCCCGCGGCCGCTGCTGCCGCCGGCGGCAGCTCGCCGTCGTCAGCCGTTTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
FIL CDNA.
Arabidopsis thaliana.
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryotta; Viridiplantae; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 966)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                               CCCTGTAATTGAGGCGGGAGGGATCTTTGCCTACGCCCGGAAGACAGGAATGATTGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTTTTCGCAACTCCGTGGCCACTGGAGAGGTGTACCCTCTGGAGCTCACGGACGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCGGTCTGTCTTGGAGCAGCTGGAGCTAAAGCCATAGTTGCTGAGTCTTACGCAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCTACGCCATCATTGTCGGCGGAGCCAACTTCGGGTGCGGTTCCTCTCGCGAGCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCGGGGCTCCCATCCGCGGCCTACCCGACGCCGTTCGTCGTCGGCTCAGGAGTGACGACTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACGGCGAGTGCTTCGTGGGGGGGACAATATCGACACCGACCAGATCATCCCCGCCGA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCCCACGTGCTGCCGCCTCAGAATCCGACTCTAACGAAGCCCTAGCCAACACAACCTT 227
                                                                                                                                                                                                                                                                                                                                           ATTAGCT
                                                                                                                                                                                                                                                                                                                                                                            GAAAGCT 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTATTGACTAATCACACGACCGGTAAAAACTATAAGCTGAAGTCGATCGGTGATGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TTTTTATTAACCACACCTCTGGCAAGGAGTACAAGCTGAAACCAATTGGTGATGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCTGGAAGGAGTGCAAGACAGGGGATGTGGTCACCGTGGACCTTGCTAACTCCG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTTTCCGTAACTCGGTTGCTACAGGAGGGGTGTTTCCGCTCGAG---TCAGAGGTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCGTCGCGCTTGGGGCCCCTGGCGCCACGCCATTGTTGCSGAGGGCTACGCGCGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGTACTCAATCATAATCGGCGGCGAAAAACTTTGGTTGCGGATCGTCACGTGAACATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCTGGTCTACCA---GACTTCCACAAAACACGGTTCATTGAGCCAGGAGAGAACAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCGCTTGCACCTTCCCATCGAACCAGCAAGAGCGTGATGAGATCGCCGCTCACGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACCTCACTCTGGTGCCCTCCAAGCCGGACGAGTACCGCAAGCTCGGTTCCTTCGCCTT 323
                                                                                                                                                                                                                                                                                                                                                                                                             ACCGGTTATTGATGCTGGTGGTATTTTTGCTTATGCGAGGATGATGGGAATGATTCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTCTGTGAGGAGTGTAAGACAGGAGATACGGTGACGATCGAGCTGAGTGATAGTGGTGG
                                                                                                                                                                                                                     Arabidopsis thaliana putative subunit (At2g43100) mRNA, comp
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Similarity 61.4%;
73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SITSRGTSSPTIEPRAAASESDSNEALANTTFHGLCYVLKDNIDTDQIIPAGAACTFP
SNQQERDEIAHALSGLPDFHKTRFIEPGENRSKYSIIIGGENFGCGSSREHAPVCLG
AAGAKAIVAESYARIFFRNSVAIGEVFPLESEVRVCEECKTGDTVTIELSDSGGLLTN
HTTGKNYKLKSIGDAGPVIDAGGIFAYARMMGMIPSLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="At2g43100"
219 c 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 197.8;
Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                        966 bp mkna arive.
attive 3-isopropylmalate dehydratase, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'UTR
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                                                                                                                                                     COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L. Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin.Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collection and clustering of RAFL cDNAs (RAFL cDNAs : (RIEEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J. Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (19-NOV-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                     260
   Conservative
                                                                                                                                                                                                                                         /Protein_id="AAL36184.1"
//db_xref="G1:7380708"
//db_xref="G1:7380708"
/translation="MAYSLPTEPQALPCSSTKTSSSLATERSPELEFNGSTSLLPSSI
/translation="MAYSLPTEPQALACTEPHECEVILKDNIDTOQIIPAGAACTEP
SITSRGTSSPTIIPRAAASESDSNEALANTTEHGLCYVILKDNIDTOQIIPAGAACTEP
SNQQEEDBIAAHALSGLPDFHKTRFIEPGENRSKYSIIIGGENGTGSSREHAPVCLG
AAGAKAIVAESYARIFERNSVATGEVEPLESEVRVCEECKTGDTVTIELSDSGGLLTN
HTTGKNYKLKSIGDAGPVIDAGGIFAYARMMGMIPSLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="This clone is in a modified pBluescript vector (Lambda ZAP) as a XhoI/SstI insert. ecotype: Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="At2g43100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="At2g43100"
15. .785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RAFL06-82-K21 (R11883)"
                                                                                                                                                     /gene="At2g43100"
234 c 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative 3-isopropylmalate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="At2g43100"
                             19.1%;
61.4%;
0;
Score 197.8; DB 8
Pred. No. 1.1e-30;
0; Mismatches 222
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                                                                                                                      Arabidopsis thaliana.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E 1 (bases 1 to 1014)

E 1 (bases 1 to 1014)

E Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,

Sowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,

Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,

Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G.,

Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,

Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K.,

Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,

Toriuml, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,

Davis, R.W., Theologis, A. and Ecker, J.R.
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Arabidopsis thaliana At2g43100/MFL8.4 mRNA,
Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
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Shinozaki, K.,
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                                                    CCGCTACGCCATCATTGTCGGCGGAGCCAACTTCGGGTGCGGTTCCTCTCGCGAGCACGC
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AAAGTACTCAATCATAATCGGCGGCGAAAACTTTGGTTGCGGATCGTCACGTGAACATGC
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RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIS.

Location/Qualifiers
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Submitted (31-OCT-2001) Salk Institute Genomic Analysis Laboratory
(SIGnAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
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Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
Davis,R.W., Theologis,A. and Ecker,J.R.
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SITSRGTSSPTLIPRAAASESDSNEALANTTFHGLCYVLKDNLOTDQILPAGAACTFP
SNQDENDEIAAHALSGLPDFHKTRFIEPGENRSKYSILIGGENFGCGSSREHAPVCLG
AAGAKALVAESYARIFFRNSVATGEVFPLESEVRVCEECKTGDTVTIELSDSGGLLTN
HTTGKNYKLKSIGDAGPVIDAGGIFAVARMMGNIPSLA"
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/product="At2g43100/MFL8.4"
/protein_id="AAL31219.1"
/db_xref="GI:16974633"
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/db_xref="taxon:3702"
/chromosome="2"
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sequencing and annotation of the RAFL cDNAs: Yamada,K., B Chang,C.H., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M. Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., M

Meyers, M.C., Miranda, M.

Jones, T.,

Lee, J.M.,

Banh, J

Stanford, PGEC (SSP) Consortium members carried out the

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Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                           Yamada, K., Banh, J., Chang, C.H., Chang, E., Dale, J.M.,
Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin, Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Meyers, M.C., Miranda, Neumann, G., Kawai, J., Kim, C., Lam, B.
Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L. Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin,Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
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1 (bases 1 to 975)
                                                                                                                                                 Submitted (04-DEC-2001) Plant Gene Expression Center, 800 Buchanan
                                                                                                                                                                         Direct Submission
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2 (bases 1
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dratase protein
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Matches
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             GATTTTCCCGTTGGA----ATCGGAGGTTAGGATTTGCGACGAGTGCAAAACAGGGGATGT
                                  GGTGTACCCTCTGGAGCTCACGGACGTTGGGGGCCTGGAAGGACTGCAAGACACGGGGATGT 593
                                                                                           AGCTGTGGTGGCGGAATCGTACGCTAGGATCTTTTTCAGGAACTGTGTAGCTACAGGTGA
                                                                                                                                CGCCATTGTTGCSGAGGGCTACGCGCGCATCTTTTTTCGCAACTCCGTGGCCACTGGAGA 533
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                                                                                                                                                                              Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs. Location/Qualifiers
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Ecker,J.R.
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/protein_id="aal38807.1"
/db_xref="g1:17529162"
/translation="MATSQQELNPTLEKSLASSNKNSGTLCPSPFLQLKSASTIFNYK
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EDREKLGSFALNGLPKEYNERRVVPGEMKSKYSVIIGGDNFGCGSSRBHAPVCLGAAG
AKAVVAESYARIFERNCVATGEIFPLESEVRICDECKTGDVVTIEHKEDGSSLLINHT
TRKEYKLKPLGDAGPVIDAGGIFAYARKAGMIPSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=experimental
/product="putative 3-isopropylmalate
small subunit"
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/db_xref="taxon:3702"
/chromosome="3"
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240 c 208 g
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17. .778
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(Lambda ZAP) as a XhoI/SstI insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RAFL06-69-M11 (R11661)"
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and T
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Theologis,A.
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Pred. No. 1.9
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REFERENCE 1 (bases 1 to 10029) AUTHORS Eisen,J.A., Nelson,K.E., Paulsen,I.T., Heidelberg,J.F., Wu,M., Dodson,R.J., Deboy,R., Gwinn,M.L., Nelson,W.C., Haft,D.H., Hickey,E.K., Peterson,J.D., Durkin,A.S., Kolonay,J.L., Yang,F., Holt,I., Umayam,L.A., Mason,T., Brenner,M., Shea,T.P., Parksey,D., Nierman,W.C., Feldblyum,T.V., Hansen,C.L., Craven,M.B., Radune,D., Vamatheyan,J., Khouri,H., White,O., Gruber,T.M., Ketchum,K.A., Venter,J.C., Tettelin,H., Bryant,D.A. and Fraser,C.M. TITLE The complete genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium photosynthetic, anaerobic, green-sulfur bacterium Proc. Natl. Acad. Sci. U.S.A. 99 (14), 9509-9514 (2002) PUBMED 1209301 REFERENCE Eisen,J.A., Nelson,K.E., Paulsen,I.T., Heidelberg,J.F., Wu,M., Dodson,R.J., Deboy,R., Gwinn,M.L., Nelson,W.C., Haft,D.H., Hickey,E.K., Peterson,J.D., Durkin,A.S., Kolonay,J.L., Yang,F.,	RESULT 14 AE012835/C LOCUS LOCUS LOCUS DEFINITION Chlorobium tepidum TLS section 56 of 194 of the complete genome. ACCESSION AE012835 AE006470 VERSION VERSION AE012835.1 GI:21646549 KEYWORDS SOURCE Chlorobium tepidum TLS Bacteria; Chlorobia; Chlorobia; Chlorobiales; Chlorobiaceae;	Qy 474 CGCCATTGTTGCCGGGAACACGCTGCAACTTTGTCTCGGCGGGGGAGCTAA 11032 Qy 474 CGCCATTGTTGCCGAAGGCTACGCGCGCATTGTTTTTTTGCCAACTTCCGGCGGGAGCTAA 11032 Qy 474 CGCCATTGTTGCCGAAGGCTACGCGGCGATTTTTTTTTGCCAACTTCCGTGGCCACTGGAGA 533	114 CCACTCACTAAAATGCCGCCGCCGCGGTCCATCGTCCCGCGGCCGCGGCCGCGCGCG
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/product="ketol-acid reductoisomerase"
/protein_id="AAM/1858.1"
/db_xref="GI:21646554"
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/gene="ilvC"
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/protein_id="aAM71857_1"
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IILAADPRRNELVKAAAGRIIDLVKKEVRPRQILTRTSMLNAFALDLAMGGSTNTILH
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IILAADSARIJDFSELNDLSAKTPYICKVSPATTEVHIEDVRAGGISAILKELSKV
EGILDLSARTVTCKTLGENIASAEVLDRYVIRSVEEPYSTTGGLAVLYGNLANGAVV
KTGAVSPAMMKHTGPAKVYDCQDDAIAGIMNGDVKSGDVVVIRYEGFRGGPGMEMLS
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/gene="ilvD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4-hydroxybutyrate dehydrogenase; NAD-dependant; lipase. Alcaligenes eutrophus (strain Hl6 SK4040) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 9830)
Valentin, H.E., Zwing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ralstonia eutropha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L36817.1 GI:695273
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1. .9830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EREARVENIVGTWPAAWNAERALALGFQSDASFDEVIRAYMEDAGLAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPAKLVNR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2107)
                                                                                                                                                                                                                                                                                                                                                                                                                 .2155)
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-10_signal
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4864. 4860
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          complement(6870.
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/transl_table=11
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signal"
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! signal"
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ORIGIN
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Best Local Similarity 52.9%;
Matches 164; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAGCCCCGATCCCTTGTTCGTGCTGAACCAGCCGGAGTACACCGGGGGCGTCGATCCTGC 8806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCTGCGCATCAACATCGACACCGACGCCATCATCCCGTCGCGGGAAATGAAGCGCGTCT 8926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCGCAACGG
                                                                                 TGGCCACTGG 530
                                                                                                                                                         AGTTCGGCATCCGCCCATCGTTGCGCCCGGCTTCGGTGCCATCTTCCACAACAACTGCG
                                                                                                                                                                                                                                               CCGCTGGCGCACGCGCATTGTTGCSGAGGGCTACGCGCGCATCTTTTTTCGCAACTCCG 520
                                                                                                                                                                                                                                                                                                                                                                                                              TCGGCGGAGCCAACTTCGGGTGCGGTTCCTCTCGCGAGCACGCGCCCCGTCGCGCTTGGGG
                                                                                                                                                                                                                                                                                                                            TGGCCGGAAGCAATTTTGGCTGCGGCTCCTCGCGCGAGCATGCGGTGTGGGGCGCTGAAGG
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NYGGLSFGGVYSLGGVAGSPARNQIWSLGAGYGSGPLLLGIGYLNVKNRNTSFYGTGV
TANTTGSAFLNTLTNIGSPVQSGYASARSQEVFAAGAAYSGAATYGTTYSNTFRNDL
GDLSSGPNPFGYRGTATFNNVEVSFKYQVTPALLMGVAADYARGSGINDASYRQFVLG
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complement(80399. .9025)
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complement(9027. .9830)
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pred. No. 1.4e-05;
1; Mismatches 145;
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Corn leuD subunit
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ALIGNMENTS

AAX89462;

CAAX89462;

AAX89462;

ST-FEB-2000 (first entry)

COrn leuD subunit of 3-isopropylmalate dehydratase nucleotide sequence.

COrn; soybean; wheat; rice; dihydroxyacid dehydratase; leuC; leuD;
branched chain amino acid transferase; biosynthetic enzyme; antibody;

CORN; soybean; wheat; rice; dihydroxyacid dehydratase; leuC; leuD;
branched chain amino acid transferase; biosynthetic enzyme; antibody;

CORN; soybean; wheat; rice; dihydroxyacid dehydratase; leuC; leuD;
branched chain amino acid transferase; biosynthetic enzyme; antibody;

CORN; soybean; wheat; rice; dihydroxyacid dehydratase; leuD;

CORN; soybean; wheat; rice; dihydroxyacid dehydratase; leuC; leuD;

CORN; soybean; wheat; rice; dihydroxyacid dehydratase; leuC; leuD;

CORN; soybean; wheat; rice; leuD;

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Matches 1033
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        GTGGACCTTGCTAACTCCGTTTTTATTAACCACACCTCTGGCAAGGAGTACAAGCTGAAA
                                                                               GTTGCSGAGGGCTACGCGCGCATCTTTTTTCGCAACTCCGTGGCCACTGGAGAGGTGTAC
                                                                                          GTTGCSGAGGGCTACGCGCGCATCTTTTTTCGCAACTCCGTGGCCACTGGAGAGGTGTAC
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         AAX89462-X89465 are fragments of corn, soybean, wheat and rice leuD subunit of 3-isopropylmalate dehydratase nucleotide sequences. Sequences AAX89442-X89465 are nucleic acid fragments that encode all or a substantial portion of dihydroxyacid dehydratase, a branched chain amino acid transferase, a leuC or a leuD subunit of 3-isopropylmalate dehydratase from wheat, corn, soybean or rice. These enzymes are involved in biosynthesis and utilization of branched-chain amino acids. The nucleic acid sequences can be used to alter the level of expression of a branched chain amino acid biosynthetic enzyme in a host cell. They can also be used to obtain a nucleic acid fragment encoding a branched chain amino acid biosynthetic enzyme. The encoded proteins may be used to prepare antibodies for detecting the proteins in situ in cells, or in vitro in cell extracts.
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Best Local Similarity
Matches 570; Conserv
                    Corn; soybean; wheat; rice; dihydroxyacid dehydratase; leuC; leuD; branched chain amino acid transférase; blosynthetic enzyme; antibody;
                                                    LeuD subunit of 3-isopropylmalate dehydratase nucleotide sequence.
                                                                              15-FEB-2000
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AACTTCGGTTGCGGCTCCTCCCGCGAGCACGCCCCCCGTCGCGCTGGGCGCCTCCGGCGCCC
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AAX89462-X89465 are fragments of corn, soybean, wheat and rice leuD subunit of 3-isopropylmalate dehydratase nucleotide sequences. Sequences AAX89442-X89465 are incleic acid fragments that encode all or a substantial portion of dihydroxyacid dehydratase, a branched chain amino acid transferase, a leuC or a leuD subunit of 3-isopropylmalate dehydratase from wheat, corn, soybean or rice. These enzymes are involved in biosynthesis and utilization of branched-chain amino acids. The nucleic acid sequences can be used to alter the level of expression of a branched chain amino acid biosynthetic enzyme in a host cell. They can amino acid biosynthetic enzyme, and to identify inhibitors of a branched chain amino acid biosynthetic enzyme. The encoded proteins may be used to prepare antibodies for detecting the proteins in situ in cells, or in vitro in cell extracts.
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AACTTCGGGTGCGGTTCCTCTCGCGAGCACGCGCCCGTCGCGCTTGGGGCCCGCTGGCGCA 471
                                                                                                                              GACGAGTACCGCAAGCTCGGTTCCTTCGCCTTCGCGGGGCTCCCATCCGGGGCCTACCCG
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                                                             ACGCCGTTCGTCGCGGTGAGGAGTCCTCCCGCTACGCCATCATTGTCGGCGGAGCC 411
                                                                                                               GACGAGTACGAGAAGCTCGGCTCCTACGCCCTCATCGGCCTCC---CCGCCACCTACGCC
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                                              ACGCGTTTCATCGAACCCGGCGAGATCAAAACCAAGTACGCCATCGTCATCGGCGGTGCC
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/product= LeuD
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/note= "Xaa = unknown"
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2000EP-0301439. 99US-0121825 99US-0123180. 99US-0125788. 99US-0126764. 99US-0127462. 99US-0128714. 99US-0130047. 99US-0130449. 99US-0131449. 99US-0132486. 99US-0132486. 99US-0132487. 99US-0132487. 99US-013486. 99US-013486. 99US-013486. 99US-013487. 99US-013487. 99US-013487. 99US-013487. 99US-013488. 99US-013488. 99US-013488. 99US-013488. 99US-013488.	GGGCCATTGTTGGGSAGGGCTACGGGGCATCTTTTTTGGCAACTCCGTGGCCACTGGA 531
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                                 AGTATTTTGATCAATCATACGACTGGGAAAGAGTATAAGCTTAAGCCGATTGGTGATGCT
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                                                                                                                                                                                                                                                                                                                                                         nutrition;
                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana; plant; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis
                                                                                                                      Garcia
Hurban
                                                                                                                                                            (ALLE/)
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(RAIN/)
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                                                                              New Arabidopsis thaliana nucleic acid for identifying homologous producing compositions that modulate the expression or function encoded protein, and mapping functional regions of protein
                                                                                                         WPI;
                                                                                                                                                                               (KRIC/)
                                                                                                                                                                                             (HAAS/)
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                                                                                                                                                      (HURB/)
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GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
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LEDFORD B L.
WOESSNER J P.
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PRICE J L.
RAINES T M.
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Page A,
Kricker N
                                                                                                                                                                                                                                                                                                                                                                                   thaliana expressed
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                                                                                                                                  Mathew AV,
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                                                                                                                             Slater
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                                                                                                                                                                                                                                                                                                                                                                 factor;
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                                                                                                                              Woessner
Allen K,
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                                                                                                                                                                                                                                                                                                                                                                        transgenic;
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                                                                                                                                                                                                                                                                                                                                                                  pathogen;
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JP, Haa
Hoffman
                                                                                                                                       Haas WD;
                                                                                        of its
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                                                                                                                                                                                                                                                                                                                                                                         stress;
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The invention relates to an Arabidopsis thaliana nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to a sequence selected from any one of 999 sequences (ABN98233-ABN99231), to a sequence selected from any one of 999 sequences (ABN98233-ABN99231), yield in the specification or its fragment. A polypeptide (II) encoded by (I), a transgenic plant (III) comprising an exogenous nucleic acid or a genetically modified cell (IV) comprising an exogenous nucleic acid, is useful for screening a candidate agent for its biological effect. (I) is useful in identifying homologous or related genes, in producing

in identifying homo. itions that modulate

expression

or

function

of its enc

Claim

1; SEQ ID NO 344; 49pp + Sequence Listing;

English

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CC programs to identify agents that mimic or enhance the action of tolerance cenhance their tolerance to environmental stress. (1) is also useful cenhance their tolerance to environmental stress. (1) is also useful compared to enhancing or inhibiting production of a biosynthetic product in a compared to proteins of interest, for establishing the extent to which car specific insect and/or pathogen is responsible for damage to a compared to a compared to a particular plant, for identifying other mediators that may induce compared to a compared 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 948
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                                           TCGAAAGCTGCTGCAT 751
                                                                                                                                                  GGGGCCTGGAAGGAGTGCAAGACAGGGGGATGTGGTCACCGTGGACCTTGCTAACTCCG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCTTTTTTCGCAACTCCGTGGCCACTGGAGAGGTGTACCCTCTGGAGCTCACGGACGTT
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RESULT 8
ABN98932
ID MAN9
XX APN9
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XX A
The invention relates to an Arabidopsis thaliana nucleic acid (I) C comprising a sequence capable of hybridising under stringent conditions CC to a sequence selected from any one of 999 sequences (ABN98233), CC given in the specification or its fragment. A polypeptide (II) encoded by C(I), a transgenic plant (III) comprising an exogenous nucleic acid or a CC genetically modified cell (IV) comprising an exogenous nucleic acid, is CC useful for screening a candidate agent for its biological effect. (I) is CC useful in identifying homologous or related genes, in producing CC compositions that modulate the expression or function of its encoded protein, mapping functional regions of the protein and in studying CC associated physiological pathways. (I) is also useful for the genetic manipulation of cells, particularly plant cells. (I) is also useful in CC care best capable of withstanding a particular disease or environmental CC stress. (II) and (III) are useful for screening of biologically active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; disease; crop; thale cress; tolerance factor: insect rathogen.
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Rameaka JG,
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GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
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MATHEW A V.

LEDFORD B L.

WOESSNER J P.
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YU Y.
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, Page A,
Kricker L
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A, Mathew AV,
er M, Slater T,
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Ledford BL, Woess
, Davis KR, Allen
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JP, Haa
Hoffman
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fman N;
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cc agents, e.g. fungicides, insecticides, etc., for elucidating biochemical cc pathways. The screened agents are useful in improved methods of treating cc crops to prevent or treat disease. (II) are also useful in screening cc programs to identify agents that mimic or enhance the action of tolerance cc factors. Such agents are useful in improved methods of treating crops to cc enhance their tolerance to environmental stress. (I) is also useful cc for enhancing or inhibiting production of a biosynthetic product in a cc plant. (III) is useful for identifying other mediators that may induce expression of proteins of interest, for establishing the extent to which cc any specific insect and/or pathogen is responsible for damage to a cc particular plant, for identifying other mediators that enhance or induce consynthetic pathways of nutritional, commercial, or medicinal value and cc particular plant, for identifying other mediators that enhance or induce to incomposite to environmental stress, for identifying factors involved in cc particular plant, for identifying other mediators that enhance or induce to incomposite the productions of nutritional, commercial, or medicinal value and cc value. (IV) is useful in the study of genetic function and regulation, cc for alteration of the cellular metabolism and for screening compounds that may affect the biological function of the gene or gene products.

Cc Note: The sequence data for this patent did not form part of the printed conscription of the printed conscription in the study of sequence.html?DocID-99909770445.
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                       TGCCTACGCCCGGAAGACAGGAATGATTGCGTC
                                                                                                        GGTCAC-----CGTGGACCTTGCTAACTCCGTTTTTATTAACCACACCTCTGGCAA
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CGCTTATGCAAGAAAAGCCGGCATGATTCCTTC
                                                                        Conservative
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Pred. No. 2.6e~32;
1; Mismatches 235;
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P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the genomic DNA region from Thermus thermophilus which contains the coding regions for the L-lysine biosynthetic protein homoaconitase hydratase subunits I and II. The gene can be used for the generation an L-lysine-producing Thermus thermophilus strain for the production of L-lysine.
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Human; DNA-binding protein; histone; chromo domain protein; chromatin organisation modifier; Y-box binding protein; DNA organisation; gene transcription; malignant disease DNA organisation; theumatic disease; genetic abnorma
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DB; AAB15394, AAB15395
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Pred. No. 0.00025;
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infectious disease; neurological disorder; gene therapy; composition of the composition o
PR 21-SEP-2000, 2000US-0234274, PR 25-SEP-2000, 2000US-02344974, PR 25-SEP-2000, 2000US-02344974, PR 25-SEP-2000, 2000US-0234987, PR 25-SEP-2000, 2000US-0234987, PR 25-SEP-2000, 2000US-0235834, PR 27-SEP-2000, 2000US-0235834, PR 27-SEP-2000, 2000US-0235834, PR 29-SEP-2000, 2000US-0235834, PR 20-CCT-2000, 2000US-0237039, PR 20-CCT-2000, 2000US-0244784, PR 20-CCT-2000, 2000US-024480, PR 20-CCT-2000, 2000US-024480, PR 20-CCT-2000, 2000US-024480, PR 20-CCT-2000, 2000US-024480, PR 20-CCT-2000, 2000US-024481, PR 20-CCT

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RESULT 11
AAS29114
ID AAS29
XX AAS29
AC AAS29
AC AAS29
XX 21-NC
XX 21-NC
XX CDNA
XX Human
KW Chrom
KW Chrom
KW DNA c
KW Linfmun
KW infmun
KW infmu
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Best Local S
Matches 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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                                                                                                                                                 Human; DNA-binding protein; histone; chromo domain protein; chromatin organisation modifier; Y-box binding protein; DNA organisation; gene transcription; malignant disease; autoimmune disorder; rheumatic disease; genetic abnormality; infectious disease; neurological disorder; gene therapy; immunomodulatory; anti-HIV; anti rheumatic; anti microbial; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS29114 standard;
                                    WO200155162-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-2001 (first entry)
                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 6.2%;
Similarity 71.2%;
84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   for human DNA-binding protein #85.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63.6; DB 22;
Pred. No. 0.00027;
D; Mismatches 34;
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22-AUG-2000;

22-AUG-2000;

23-AUG-2000;

31-AUG-2000;

01-SEP-2000;

01-SEP-2000;

01-SEP-2000;

01-SEP-2000;

05-SEP-2000;

06-SEP-2000;

06-SEP-2000;

08-SEP-2000;

08-SEP-2000;
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04-FEB-2000;
24-FEB-2000;
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26-JUL-2000;
26-JUL-2000;
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07-JUL-2000;
07-JUL-2000;
         14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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14-AUG-
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14-AUG-2000;
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                                                                        2000US-022515.
2000US-021515.
2000US-0214886.
2000US-0216887.
2000US-0216887.
2000US-0216887.
2000US-0217487.
2000US-0217487.
2000US-0224518.
2000US-0224519.
2000US-0225213.
2000US-0225266.
2000US-0225266.
2000US-022575.
2000US-0225770.
2000US-0225779.
2000US-0225779.
2000US-0225779.
2000US-0225779.
2000US-0225758.
2000US-0225758.
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2000US-0225758.
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2000US-0225758.
2000US-0225758.
2000US-0225759.
2000US-0235744.
2000US-0235745.
2000US-0235747.
2000US-0235747.
2000US-02357484.
2000US-02357484.
2000US-0235836.
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29-SEP-2000
29-SEP-2000
29-SEP-2000
20-CCT-2000
20-CCT
WPI; 2001-465557/50
                                                             Rosen CA,
                                                                                                                        HUMAN
                                                             Barash SC,
                                                                                                                                                                                      2000US -024 1221
2000US -024 1221
2000US -024 1785
2000US -024 1808
2000US -024 1808
2000US -024 6475
2000US -024 6528
2000US -024 6528
2000US -024 6528
2000US -024 6528
2000US -024 6610
2000US -024 6610
2000US -024 6611
2000US -024 9207
2000US -024 9216
2000US -024 9217
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2000US-0236369
2000US-0236370
2000US-0236802
2000US-0237037
2000US-0237038
2000US-0237039
2000US-0237039
2000US-0239935
2000US-0239935
2000US-0239935
2000US-0239935
                                                                                                                           GENOME
                                                                                                                           SCI
                                                          Ruben SM;
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Similarity

6.2%;

Length

297;

0;

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The present invention relates to the isolation of novel DNA-binding proteins (AAU18154-AAU18281), and cDNA and genomic sequences encoding for these proteins. DNA-binding proteins such as histones, chromo (chromatin organisation modifier) domain proteins, and Y-box binding proteins may contribute to diseases resulting from aberrant DNA crystalian and/or gene transcription. The sequences of the invention are useful in screening assays to identify antagonists and/or agonists that may enhance or block activities mediated by DNA-binding proteins. Blockers of DNA-binding proteins may be useful in treating disorders such as malignant diseases (e.g. cancer), autoimmune disorders (e.g. diabetes mellitus), rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological disorders (e.g. Alzheimer's disease). The polynucleotide sequences of the invention may also be used in gene therapy. AAS29030-AAS29157 represent cDNA sequences on over DNA-binding proteins.

Note: The sequence data for this patent did not form part of the printed at first transport of the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU18238
Sequence 297 BP; 129 A; 47 C;
                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95; 561pp; English.
  51 G; 68 T; 2 other;
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Best Local S
Matches 84
                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                            Human polynucleotide SEQ ID NO
                                                                                                                                                                            06-NOV-2001
                                                                                                                                                                                          AAI89088;
                                                                                                                                                                                                         AAI89088 standard; cDNA; 387
                                                                                                                                                                                                                                               208
                                                                                                                                                                                                                                                              976
                                                                                                                                                                                                                                                                            148
                                                                                                                                                                                                                                                                                           916
                                                                                                                                                                                                                                               TITITITGTTACTAGTACTTGTACAATIGTACTCCTGCCTGCTACTGTTCTTATCTGTTTG 975
                                                                                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                         Score 63.6; DB 22;
Pred. No. 0.00029;
0; Mismatches 34;
                                                                                                                                                                                                         ВP
                                                                                                                                                            9148.
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                                                                                                                                                                                                                                                                                                         0;
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28-FEB-2000; 2000US-0515126 18-MAY-2000; 2000US-0577409

26-FEB-2001; 2001WO-US04927.

WO200164835-A2 Homo sapiens. nervous

system

disorders;

Tang YT,

Liu C, Drmanac

RT;

(HYSE-)

HYSEQ INC

Claim

4.

SEQ ID

Ö 2;

3pp + Sequence Listing; English.

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RESULT 13
AA199683/c
ID AA1996
XX AA1996
XX AA1996
XX Mycoba
XX Mycoba
XX Mycoba
XX Mycoba
XX Mycoba
XX Wycoba
XX US6294
XX Wycoba
XX Wycoba
XX Mycoba
XX Mycoba
XX Mycoba
XX Wycoba
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XX Fleisc
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P-PSDB;
                             Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                                                                             Fleischmann RD,
                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6294328-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis strain H37Rv genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI99683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI99683 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 9148; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing and treating e.g.
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                                                                                                                                                                                                                                                                                   (GENO-) INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation.
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DB; AAO09157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ium tuberculosis; strain H37Rv; strain CDC 1551; genome
epidemiology; patient treatment; epidemic monitoring;
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                                                                                                                                                                                                                                                                                   GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis
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                                                                                                                                                                                                                             White OR,
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Pred. No. 0.0057;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37RV (AAI99683). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of M. tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                         Nematode; transglutaminase; nematocide; Dirofilaria immitis; Brugia malayi; Onchocerca volvulus; antinematode vaccine; ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6294328B1.
07-MAY-2002
                                                                                                                                                               Dirofilaria immitis transglutaminase gene
                                                                                                                                                                                                                                                                               ABK82308 standard; cDNA; 1466
                                     US6383774-B1
                                                                     Dirofilaria immitis
                                                                                                                                                                                                       27-AUG-2002
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RESULT 15
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XX Dirof
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XX Brugi
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid (I) encoding nematode transglutaminase. (I), optionally incorporated into recombinant viruses or cells, are used to treat or prevent infestation by parasitic nematodes in humans or animals, especially by Dirofilaria immitis, Brugia malayi or Onchocerca volvulus. (I) can also be used for expression of the corresponding recombinant proteins which are also useful in antinematode vaccines and for raising antibodies (useful for treatment or diagnosis). ABK82304-ABK82347 represent nematode transglutaminase
                                    03-DEC-1996;
12-JUN-1997;
                                                                                                                                                                        Nematode; transglutaminase; nematocide; Dirofilaria immitis; Brugia malayi; Onchocerca volvulus; antinematode vaccine; ge
                                                                                                                                                                                                                 Dirofilaria
                                                                                                                                                                                                                                                                                         ABK82309 standard; cDNA;
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                                                                         04-DEC-1997;
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                                                                                                                         US6383774-B1
                                                                                                                                                  Dirofilaria immitis
                                                                                                                                                                                                                                        27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1345 TTTTGTTTACCTTATGTTACTGTTGTTATTGTATTACTATTTTGCCCCTTGTTTTTTTAAAT 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1466 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Column 61-63; 66pp;
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12-JUN-1997;
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             (HESK-) HESKA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid encoding nematode transglutaminase, useful in vaccines treating or preventing nematode infestation in humans and animals
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97US-0874102.
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97US-0874102
                                                                         97US-0984919
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                                                                                                                                                                                                              transglutaminase gene #6.
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Pred. No.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid (I) encoding nematode transglutaminase. (I), optionally incorporated into recombinant viruses or cells, are used to treat or prevent infestation by parasitic nematodes in humans or animals, especially by Dirofilaria immitis, Brugia malayi or Onchocerca volvulus. (I) can also be used for expression of the corresponding recombinant proteins which are also useful in antinematode vaccines and for raising antibodies (useful for treatment or diagnosis). ABK82304-ABK82347 represent nematode transglutaminase coding sequences and primers of the invention.
                                                                                           1033 A 1033
                                                                                                                                                                                                                                                                                                             Sequence 1466 BP; 440 A; 297 C; 209 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
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                                                                                                                                                                                                                                                                Similarity
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Sequence 122, App
Sequence 112, App
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 95, Appl
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APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC
FILE REFERENCE: BB-1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; S
Best Local Similarity 100.0%; F
Matches 1033; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/027,450 CURRENT FILING DATE: 2001-12-20 PRIOR APPLICATION NUMBER: 60/063,423 PRIOR FILING DATE: 1997 October 28 NUMBER OF SEQ ID NOS: 54
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	237.	63. A	Sequence 237, App	63, 7	•	Sequence 237, App	63, 1	Sequence 451, App	25,	e 25,	25,	l, Apr	Sequence 118, App	e 150	13, /	Sequence 317, App	e 1,	Ą	Sequence 577, App	Sequence 289, App	606,	606,	31,	Sequence 490, App	Sequence 478, App	Sequence 4845, Ap

ALIGNMENTS

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121 CTAAAATGCCGCCCGCGCTCGGTCCATCCTCCCCGCGGCGCGCTGCTGCCGCGCGGCAGC 180
                                                                                                          AGCTCGCCGTCGTCAGCCGTTTTCCACGGCGAGTGCTTCGTGGTGGGCGACAATATCGAC
                                             CTAAAATGCCGCCGCGCTGGGTCCATCGTCCCCGCGGCCGCCTGCTGCCGCGGCGGCAGC 180
Score 1032.6; DB 12; Length 1033;
Pred. No. 3.6e-275;
); Mismatches 0; Indels 0; G
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US-10-07-450-52
US-10-07-450-52
Sequence 52, Application US/10027450
Patent No. US20020102715A1
GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMI
FILE REFERENCE: BB-1126
CURRENT APPLICATION NUMBER: US/10/027,450
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCGCTCCGGGTGAGGAGTCCTCCCGCTACGCCATCATTGTCGGCGGAGCCAACCTTCGGGGTCACCTCCGGGTCACGCCATCATTGTCGGCGGAGCCAACCTTCGGGGTCACCTCCCGCTACGCCATCATTGTCGGCGGAGCCAACCTTCGGG
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; TYPE: DNA
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US-10-027-450-52
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Best Local Similarity 99.0%;
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October 28
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1; Mismatches
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APPLICANT: Falco, Saverio Carl
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Bafalski, J. Antoni
CURRENT ELING DATE: 126
PRIOR APPLICATION NUMBER: US/10/027,450
CURRENT FILING DATE: 1901-12-20
PRIOR FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 48
LENGTH: 1112
TYPE: DNA
ORGANISM: Oryza sativa
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US-10-027-450-48
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Best Local Sim
Matches 570;
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Matches
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APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50, Applica Patent No. US2002010 GENERAL INFORMATION:
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430; Conserv
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TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES FILE REFERENCE: BB-1126
CURRENT APPLICATION UNMERS: US/10/027,450
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/063,423
PRIOR FILING DATE: 1997 October 28
SUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 50
LENGTH: 1107
                                                                                                                                                                                                                                                                                                                                                                                      GACGAGTACCGCAAGCTCGGTTCCTTCGCCTTCGCGGGGCTCCCATCCGCGGCCTACCCG
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                                                           TCCGCCGCGTCCGCTTCTCCCCTCCGCCTTCCCACGGCCTCTGCTACGTCGTCGGCGAC
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                                                                                                                                                                                  GACGAGTACGAGAAGCTCGGCTCCTACGCCCTCATCGGCCTCC---CCGCCACCTACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 291.2; DB 12;
Pred. No. 2.1e-70;
1; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1107;
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS,
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                          GAGTTTCTCACTCCTCCCTTCGAATCCAGAGGAATACGAGAAACTCGGTTCTTACGCT
                                                                                                                                                                                                                                       GAGCACCTCACTCTGGTGCCCTCCAAGCCGGAGCAGTACCGCAAGCTCGGTTCCCTTCGCC 321
ATCTTTTTCAGGAACTCTGTTGCTACTGGTGAGGTTTATCCTTTGGATT---CTGAAGTT
                 ATCTTTTTCGCAACTCCGTGGCCACTGGAGAGGTGTACCCTCTGGAGCTCACGGACGTT 561
                                                       GCTCCGGTTTGTTTAGGAGCAGCGGGAGCTAAAGCAGTGGTGGCTCAGTCTTATGCTAGA
                                                                        GCGCCCGTCGCGCTTGGGGCCGCTGGCGCGCCACTGCTTGCCGCGGGCTACGCGCGC 501
                                                                                                             ACGAAGTACTCAATCATTGGCGGTGAAAACTTTGGATGTGGATCGTCACGTGAACAT 444
                                                                                                                                                                    TTAGTTGGTCTTCCA---GCTTCTTACAAGGAACGATTCGTTCAGCCAGGTGAGATGAAG
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milarity 65.2%;
Conservative
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US-09-770-445-344
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APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US / ^ CURRENT APPLICATION:
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                                                                                                                                                                                                                                                                                           SEQ ID NO 344
LENGTH: 948
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Best Local S
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CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEC ID NOS: 999
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                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                                                                                                  262 GAGCACCTCACTCTGGTGCCCTCCAAGCCGGGCGACGACGAGCAGCAGCTCGGTTCCCTTCGCC
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                                                                                  TTAGTTGGTCTTCCA---GCTTCTTACAAGGAACGATTCGTTCAGCCAGGTGAGATGAAG
                                                    TTCGCGGGGCTCCCATCCGCGGCCTACCCGACGCCGTTCGTCGCTCCGGGTGAGGAGTCC
                                                                                                                                                                                                361;
                                                                                                                                                                                                             Similarity
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Price, Jennifer L
Raines, Tracy M.
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Slader, Ted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis, Keith R.
Allen, Keith
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Rameaka, Joshua G
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                                                                                                                                                                                                               Score 209.2; DB 1 pred. No. 8.5e-48;
                                                                                                                                                                                                   Mismatches
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APPLICANT: Kreps, Joef
APPLICANT: Kreps, Joef
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Jhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: U
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1335, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                  Match 19.1%; Score 197.8; DB 9; Local Similarity 61.4%; Pred. No. 1.1e-44; les 373; Conservative 0; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGCCTGGAAGGAGTGCAAGACAGGGGATGTGGTCACCGTGGAACCTTGCTAACTCCG--
                           CGCGGGGCTCCCATCCGCGGCCTACCCGACGCCGTTCGTCGCTCCGGGTGAGGAGTCCTC 383
                                                                                                                                                                      CCACGGCGAGTGCTTCGTGGTGGGCGACAATATCGACACCGACCAGATCATCCCCGCCGA 263
                                                                                                                                                                                                                                   CATCCCACGTGCTGCCGCCTCAGAATCCGACTCTAACGAAGCCCTAGCCAACACAACCTT
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                                                                                                         GCACCTCACTCTGGTGCCCTCCAAGCCGGACGACTACCGCAAGCTCGGTTCCTTCGCCTT 323
                                                                                                                                                  CCACGGCCTCTGCTATGTCTTGAAAGACAACATAGACACCGACCAGATCATCCCAGCAGG 287
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    Indels 12;
                                                                                                                                                                                                                                                                                                                                                           Length 771;
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                                                                                     ; ORGANISM: Arabidopsis thaliana US-09-770-445-700
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US-09-770-445-700
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Query Match
Best Local Similarity 60...
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                                                                                                                                                                    SOFTWARE: F
SEQ ID NO 700
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Expressed Sequences TITLE OF INVENTION: thaliana FILE REFERENCE: 2023US (PARA-012PRV)
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                                                                                                                           TYPE: DNA
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                                                                                                                                                                                           FastSEQ for Windows Version 4.0
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
                                                                                                                                                                                                                                                                                                                                                                                 Hoffman, Neil
Hurban, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                        Davis, Keith R. Allen, Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Slader,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kricker, Maja
Slader, Ted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garcia, Carlos A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yu, Yang
Rameaka, Joshua G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page, Amy
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                      19.0%;
  Score 196.6; DB 1
Pred. No. 2.4e-44;
1; Mismatches 235
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                                             DB 10;
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                                             829;
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    Gaps
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APPLICANT: Byrun, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION UMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NO 157
SEQ ID NO 157
SEQ ID NO 157
CENCTH: 369
TYPE: DNA
ORGANISM: Glycine max
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-054-Q1-B1-E8
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 Query Match
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                                                                                                                                                                                                                                                                                                                                                         Sequence 157, Application US/09878574 Patent No. US20020110548A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCAGCAGCTCGCCGTCGTCAGCCGTTTTTCCACGGCGAGTGCTTCGTGGTGGGCGACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCAGGCGAGTCAATAACCAGAGAGACTTTCCACGGCCTCTGCTTCGTCTTGAAAGACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAATACAAACTGAAAACCGCTCGGTGATGCCGGTGCCGGTGATCGACGCCGGTGGAATCTT
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               18.1%;
70.8%;
Score 187.2; DB 10;
Pred. No. 5.9e-42;
1; Mismatches 104;
                                Length
                                  369;
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   Gaps
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ORGANISM: Glycine of the organism of the organ
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APPLICANT: Tha Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules an

TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/33,535

PRIOR FILING DATE: 1999-06-14

PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-878-574-1701
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SEQ ID NO 1701
LENGTH: 373
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                               295
                                                                                                                                                                                                                                                                                                                                                                                  175 CGGCGCGTCCGCCTCCCTTCCATGGCCTCTGCTACGTCGTCGGCGACAACATCGA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AAAACCGGCA 369
                                                          360 CGTCGCTCCGGGTGAG 375
                                                                                                                                                                                                                                                              235 GACCGATCAGATGATTCCCGCGGAGTAGCTCACCCTCGTCCCTTCGAAGCCCGACGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGGTCGCGAGTCGTACGCTAGGATCTTCTTTCGGAACTCCGTGGCCACCGGCGAGGTG
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CGTCGACCCCGGCGAG
                                                                                                                           CGAGAAGCTCGGCCCTACGCCCTCGTCGGCCTCC---CCGCCACCTAGGCCGCGCGTT
                                                                                                                                                             CCGCAAGCTCGGTTCGCCTTCGCCGGGGCTCCCATCCGCGGCCTACCCGACGCCGTT 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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: Clone ID: LIB3028-034-Q1-B1-E6
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367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 96.8; DB 10;
Pred. No. 5.5e-17;
0; Mismatches 52;
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APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 123
LENGTH: 218
TYPE: DN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                       ; TYPE: DNA; ORYGINE max; OTHER INFORMATION: Clone ID: LIB3028-055-Q1-B1-E5US-09-878-574-122
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-055-Q1-B1-E6
US-09-878-574-123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-878-574-122
                                                            Query Match
Best Local S
Matches 123
                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SEQ ID NO 122
LENGTH: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 122, Application US/09878574 Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                                          APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (15401)8
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 125;
358 TTCGTCGCTCCGGGTGAGGAGTCCTCCCGCTACGCCATCATTGTCGGCGGAGCCAACCTTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 GTCTC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           538 TACCC 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 GTGGTCGCGGATTCGTGCGCTACGATCTTCTTTCGGGACTCCGTGGAGACCGGCTAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 TICGICGCTCCGGGTGAGGAGTCCTCCCGCTACGCCATCATTGTCGGCGGAGCCAACTIC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 GGGTGCGGTTCCTCTCGCGAGCACGCGCCCCGTCGCGCTTGGGGCCCCCTGGCGCACGCGCC 477
                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GETTGCAGCTCCTCCCGCGAGCACGCGCGCGCGCGCTGGGCGCGCCTCAGGCGCCGCCGCCGA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TACATCGAATCCGGCGAGATCAAAGTCAAGTACGCCATCGTCATCGGCGGTGCCACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGTTGCSGAGGGCTACCGCGCGCATCTTTTTTCGCAACTCCGTGGCCACTGGAGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                              Conservative
                                                                             8.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.7%;
                                                          Score 88.8; DB 10;
Pred. No. 5.9e-15;
1; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 90.2; DB 10;
Pred. No. 2.7e-15;
1; Mismatches 59;
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                                                                                               Length 185;
                                                            Indels
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Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 348
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
ENGTH: 217
TYPE: DNA
DRAANISM: Homo sapiens
US-09-764-846-18
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-091-483-18
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US-10-091-483-18
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/09764846 Patent No. US20020102638A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/10091483 Publication No. US20030049650A1 GENERAL INFORMATION:
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Best Local Similarity 71.2%;
Matches 84; Conservative
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                                                                                      Query Match
Best Local Similarity
                                                                         Matches
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ12
FILE REFERENCE: PTZ12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/091,483
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 348
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior Application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ12C1
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

JOURNAL REFERENCE AUTHORS TITLE JOURNAL DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS RESULT 1 AY109732 LOCUS FEATURES TITLE Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Unpublished (2002)
2 (bases 1 to 1085)
Coe,E.C.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1. 1085 Zea mays. Zea mays Zea mays CL1042_1 mRNA sequence. AY109732 AY109732.1 GI:21213564 HTC. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. AY109732 (bases 1 to 1085) /organism="Zea mays"
/db_xref="MaizeDB:629913"
/db_xref="taxon:4577"
/clone="CL1042_1" 1085 bp mRNA linear HTC 25-MAY-2002

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BASE COUNT
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a 303 c 295 g 239 t 45 others
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                                                                                                               ACGCGCCATTGTTGCGGAGGGCTACGCGCGCATCTTTTTTCGCAACTCCGTGGCCACTGG
                                                                                                                          ACGCGCCATTGTTGCSGAGGGCTACGCGCGCATCTTTTTTCGCAACTCCGTGGCCACTGG
                       TGTGGTCACCGTGGACCTTGCTAACTCCGTTTTTATTAACCACACCTCTGGCAAGGAGTA
                                                                               AGAGGTGTACCCTCTGGAGCTCACGGACGTTGGGGCCTGGAAGGAGTGCAAGACACGGGGA
 AGAGGTGTACCCTCTGGAGCTCACGGACGTTGGGGCCTGGAAGGAGTGCAAGACAGGGGA
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Department of Biological Sciences
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Plate: 496028 row: H col
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70; Conservative
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: 650 723 2227
:: 650 725 8221
                                                                                                                                                                                                                                                                 150
                                                                                                                                                                                                                                                               /tissue_type="seedling"
/dev_stage="salt stress"
/lab_host="E.coli XL Gold"
/note="organ: shoot; Vector: pi
Wang/Bohnert"
wang/Bohnert"
162 c 135 g 124 t
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/tlsana +---
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/clone_lib="496 - str
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/cultivar="B73"
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Pred. No. 4.4e-82;
1; Mismatches 0
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            GCCTGCTACTGTTCTTATCTGTTTTGAATAAC 981
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                                                                   al Similarity
539; Conser
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855 California Ave, Palo Alto,
723 227
Tel: 650 725 8221
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 546)
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AI820332
AI820332.1 GI:54394
                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Walbot V
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605091F07.yl 605 - Endosperm
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                                                                                                                                  76
                                                                   Conservative
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605091 row: F col
                                                                                                                                  Ø
                                                                                                                                                               /organism="Zea mays"
/cultivar="Ohio43"
/cultivar="Ohio43"
/db_xref="faxon:4577"
/clone_lib="605 - Endosperm cDNA library from Schmi/
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/lab_host="DH5(alpha)"
/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1:
/note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1:
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Site_2: XhoI; Kernel endosperm
                                                                                                                                              lab
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                                                                             51.9%;
98.7%;
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Department of Biological S
Stanford University
855 California Ave, Palo A
Tel: 650 723 2227
Fax: 650 725 8221
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 589)
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AI833533
                                                                                                                                                                                                                                    Unpublished (1999)
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                                                                                                                               walbot@stanford.edu
605091 row; F col
         /organism="Zea mays"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/clone_lib="605 - Endosperm cDNA library
/clone_lib="605 - Endosperm cDNA library
/tissue_type="nucellar, embryo, and endos
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
                                                                                                             Location/Qualifiers
 /note="Organ: Kernel;
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Vector: pAD-GAL4-2';
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 University
Unpublished (1999)
Contact: Walbot V
Department of Biological s
Stanford University
855 California Ave, Palo P
Tel: 650 723 2227
                                                                                                                                                                                        946053608.y1 946 - tassel | mays cDNA, mRNA sequence. BE510562 BE510562.1 GI:9731810 EST.
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                 GGTCTTTGTCACAGAT 910
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                                                                                                                                                    CCTCTGCGGAGATGAAGAAGTAAGCTGGAGTTAGGACTAAGAGTTACTGCACCTACTTGA 834
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l: walbot@stanford.edu
e: 946053 row: G col
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/cultivar="0H43"
/db_xref="taxon:4577"
/clone_lib="946 - tass
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1 141 c 170 g 125 t 1 others
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/dev_stage="just after the
inflorescence development"
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Pred. No. 4.9e-75;
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TGAATCAATCAATTTGGTCTTTGTCACAGATCGTTTTTT--TTTGTTACTAGTACTTGTA 937
                                                                                                                                                                        TGCCTACGCCCGGAAGACAGGAATGATTGCGTCGAAAGCTGCTGCATGAGGGAA-----A
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                                                          ACTGCACCTACTTGATGTCGACGGTGTCTCAAAATAAGTTGCGGCCTACCGAAATTATGA 879
                                                                                                  GCTTATGCAGCCGAGCCTCTGCGGAGATGAAGAAGTAAGCTGGAGTTAGGACTAAGAGTT 819
                                                                                                                                                          TGCCTACGCCCGGAAGACAGGAATGATTGCGTCGAAAGCTGCTGCATGAGGGAAAGATCA
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Plate: 946053 row: G column:
Location/Qualifiers
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855 California Ave, Palo Alto,
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Contact: Walbot V
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154 c 129 g 130 t
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/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassel
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/dev_stage="just after the
inflorescence development"
/lab_host="XLOLR"
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Pred. No. 1.1e-69;
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                                                                                                                                                                                                                                         GGAATGATTGCGTCGAAAGCTGCTGCATGAGGGAA-----AGCTTATGCAGCCGAGCCTC
                                                                           ATTGGTGATGCTGGCCCTGTAATTGAGGCGGGAGGGATCTTTGCCTACGCCCGGAAGACA 723
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TGCGGAGATGAAGTAAGCTGGAGTTAGGACTAAGAGTTACTGCACCTACTTGATGTC
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AI677354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: walbot@stanford.edu
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                                                                                                                                                                                                                                                                                                                                                                 172
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        /note-"Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: Site_2: XhoI; Kernel endosperm cDNA library from Sc
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/cultivar="0hiod3"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="605 - Endosperm cDNA library from
/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
                                                                                                                                                                                                                                                                                                                                                                              lab"
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Pred. No. 2.6e-66;
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a; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Sciences Building, Rm. 2502, Athens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Spermatophyta; Magnoliophyta; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An EST database from Sorghum: 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PI1_60_D05.b1_A002 Pathogen mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clade; Panicoideae; Andropogoneae;
1 (bases 1 to 534)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE597022.1
                                            95
                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop:
                                                                                                                /clone_llb="Rethogen induced 1 (PII)"
/clone_"llb="Rethogen induced 1 (PII)"
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda Zap II. Clones to be
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                                                                       sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                           the
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                       organism="Sorghum bicolor"
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                                          pathogen.
173 c
45.7%;
Score 471.6;
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                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Plant m. 2502, Athens, GA
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GA 30602-7271,
Length 534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 AAGCCGGACGAGTACCGCAAGCTCGGTTCCTTCGCCTTCGCGGGGCTCCCATCCGCGGCC 345
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                                                                                                sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
                                                                                                                                                                                                                         Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA
                                                                                                                                                                                                                                                                                                                          An EST database from Sorghum:
                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 564)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.,
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sorghum.
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE360232 564 |
DG1_62_G01.b1_A002 Dark Grown
                                                         Seq primer: JEN REV
High quality sequence
                                                                                                                                          Email: mmpratt@uga.edu
Sequences have been tri
                                                                                                                                                                                Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                         Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE360232.1
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Location/Qualifiers
1. .564
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1; Mismatches 35;
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Grown 1
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                                                                                                                                                                                                                              lant Biology
GA 30602-7271,
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REFERENCE
AUTHORS
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ORGANISM
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VERSION
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AW677919
                                            COMMENT
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497; Conserv
                                                                                                                                                                                                                AW677919
WS1_12_D01.b1_A002 W
mRNA sequence.
AW677919
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 566)

Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                               Sorghum bicolor
                                                                                                                                                                           sorghum.
                                                                  EST database from Sorghum:
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/db_xref="taxon:4558"
/clone_lib="bark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhOI; Site_2: EBOORI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 223 c 170 g 98 t
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1 (WS1) Sorghum
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bicolor cDNA,
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Best Local
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176 GCAGCAGCTCGCCGTCGTCAGCCGTTTTTCCACGGCGAGTGCTTCGTGGTGGGCGACAATA 235
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                                                                                                                                                                                                             TGAAACCAATTGGTGATGCTGGTCC
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OVI_28_C06.b1_A002 (

sequence.

BG047825.1 GI:12497

BG047825.1 GI:12497
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Sequences have been trimmed
below Phred quality 16. The
sorghum
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Fax: 706 583 0210
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Similarity 93.5%;
72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop:
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/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
196 c 165 g 112 t
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/db_xref="taxon:4558"
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Ovary 1 (
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                                                                                          mRNA linear
Sorghum bicolor
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Best Local Similarity
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                                                                                                               ACTCCGTTTTTATTAACCACACCCTCTGGCAAGGAGTACAAGCTGAAACCAATTGGTGATG
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Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Pantocideae; Andropogoneae; Sorghum.

1 (bases 1 to 551)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: JEN REV
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Ovary I (OV1)"
/note="Organ: Mix of ovaries of varying immature stages from 8-week-old plants; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. clones to be sequenced were prepared by mass excision."

a 170 c 175 g 110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 453; DB 12;
Pred. No. 2.9e-63;
I; Mismatches 36;
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Sorghum bicolor
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Tel: 706 542 1860
Fax: 706 583 0210
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DG1_62_B02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
Sequences have been tr
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milarity 91.6%;
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GACACCGACCAGATCATCCCCGCCGAGCACCTCACTCTGGTGCCCTCCAAGCCGGACGAG CTAAAATGCCGCCGCGCTGGGTCCATCGTCCCCGCGGCCGCCGCTGCTGCCGCGGCGG----GC CGAGCTCCAACCAGCGCTTTATCCGGCGCTCCCAGCTCACCTGTCATCGCCTCCACTCA 120 ATCATGGCGGCGCTCTGTCGGGGACGGCGGTGTCCACGGCAGCGCTTCTAGCCCCAATC 60 TACCGCAAGCTCGGCTCCTTTGCCTTCGCGGGGCCTCCCCTCCGCGGCCTACCCGACGCCG TACCGCAAGCTCGGTTCCTTCGCCTTCGCGGGGCTCCCCATCCGCGGCCTACCCGACGCCG AGCAGCTCGCCGTCGTCAGCCGTTTTCCACGGCGAGTGCTTCGTGGTGGGCGACAATATC CGAGCTCCAACCAGCGCGTTTCTCCGGCGCACCCAGCTCACCCGTCACCGCGACCACTCC 143 Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 546) Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., /Clone_lib="Dark Grown 1 (DG1)"
note="organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EccRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 220 c 162 g 94 t /organism="Sorghum bicolor" /db_xref="taxon:4558" Score 442.6; DB 1 Pred. No. 1.4e-61; 1; Mismatches 40 512 to exclude PolyA, vector and regions threshold for highest quality sequence n 1 dark-grown seedlings mRNA linear EST 20-JUL-2000 (DG1) Sorghum bicolor cDNA, mRNA DB 10; 40; Indels Length Sudman, M. ζ, Gaps 177 83 263 237 357 323 297 203 1;

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RESULT 13
BG309960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; Elliopsida; Poales; Triticeae; Hordeum.

1 (bases 1 to 841)
Wing, Colors
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Seq primer: AATTAACCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare
Eukaryota; Viridiplantae;
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/note="Vector: lambdaZAP: Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five day old seedling shoots were then harvested, total RNA was propared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of california, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Clone_11b="Hordeum vulgare seedling shoot EST library HVCDNA0003 (Etiolated and unstressed)" /tissue_type="Seedling shoot" /lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HYSMEC0015H22f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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RESULT 14 AW747153

ACCESSION DEFINITION

mRNA sequence. AW747153

GI:7660891

AW747153 534 bp mRNA linear EST 19-JUL-WS1_66_G07.b1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA.

EST 19-JUL-2000

VERSION

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                              GCTGC 746
                                                                          GTAATTGAGGCGGGAGGGATCTTTGCCTACGCCCGGAAGACAGGAATGATTGCGTCGAAA 741
                                                                                                                                                                                                              GGGGCCTGGAAGGAGTGCAAGACAGGGGATGTGGTCACCGTGGACCTTGCTAACTCCGTT 621
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                                                                                                                     TTTATTAACCACACCTCTGGCAAGGAGTACAAGCTGAAACCAATTGGTGATGCTGGCCCT 681
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Pred. No. 1.5e-
1; Mismatches
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CTTTGCCTATGCTCGGAAGACAGGAATGATCGCGTCAAAAGCTGCTGCATGAGGGAAAGG
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sorghum.
sorghum bicolor
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1 (bases 1 to 534)
Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,L.H.
An EST database from Sorghum:
Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
a 158 c 172 g 108 t
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/db_xref="taxon:4558"
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Pred. No. 2.2e-59;
1; Mismatches 53;
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                           GGAGATGAAGAAGTAAGCTGGAGTTAGGACTAAGAGTTACTGCACCTACTTGATGTCGAC
                                                                                                   ATGATTGCGTCGAAAGCTGCTGCATGAGGGAA-----AGCTTATGCAGCCGAGCCTCTGC
                                                                                    ATGATTGCGTCGAAAGCTGCTGCATGAGGGAAAGATCAGCTTAGGCAGCCGAGCCTCTGC
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BG267153
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Spermatophyta; Magnoliophyta; Liliopsida; Poales;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 500)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                855 California Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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Plate: 1000112 row: B co
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Location/Qualifiers
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/db_xref="dbEST:605053H06.x1"
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Pred. No. 8.9e-57;
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2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-173-300-52
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US-08-984-919A-12
US-08-984-919A-12
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US-08-874-102-12
US-08-984-919A-12
US-08-984-919A-48
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Sequence 46, Appl Sequence 52, Appl Sequence 20, Appl Sequence 10, Appl Sequence 11, Appl Sequence 46, Appl Sequence 46, Appl Sequence 48, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 21, Appl Sequence 11, Appl Sequence 11,
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CCCATCCG	CACTCTGGTGCC	GTGCTTCG	99006 	CCAGCTCAC 	CACGG CACGG	1032.6; D No. 4.7e-2 natches	300	ENTS	9-099-041A-25 9-245-281-25 9-245-281-25 8-800-339-75 8-804-2970-5 8-804-198-1 9-149-4-64 9-149-4-64 9-149-4-64 9-149-4-64 9-149-4-64 9-149-4-64 9-159-2118-24 9-005-051-26 9-005-051-26 9-005-051-26 9-159-35-35 8-446-855A-1 9-150-741-1
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RESULT 2
US-09-173-300-52
US-09-173-300-52
Sequence 52, Application US/09173300
Patent No. 6451581
GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMI
FILE REFERENCE: BB-1126
CURRENT APPLICATION NUMBER: US/09/173,300
CURRENT APPLICATION NUMBER: 60/063,423
EARLIER APPLICATION NUMBER: 60/063,423
EARLIER FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 52
LENGTH: 995
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GENERAL INFORMATION:

APPLICANT: Falco, Saverio Carl

APPLICANT: Kinney, Anthony J.

APPLICANT: Kinney, Anthony J.

APPLICANT: Kinney, Anthony J.

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Cafosh, J. Antoni

TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC EN

FILE REFERENCE: BB-1126

CURRENT APPLICATION NUMBER: US/09/173,300

CURRENT APPLICATION NUMBER: 60/063,423

EARLIER FILING DATE: 1998-10-15

EARLIER FILING DATE: 1997 October 28

NUMBER OF SEQ ID NOS: 54

SOFTWARE: Microsoft Word Version 7.0A
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LENGTH; 1112;
TYPE: DNA;
ORGANISM: Oryza sativa
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                                                                                                              GCGCATCTTTTTTCGCAACTCCGTGGCCACTGGAGAGGTGTACCCTCTGGAGCTCACGGA 557
                                                                                                                                                             GCACGCGCCCGTCGCGCTTGGGGGCCGCGGGGGCATTGTTGCSGAGGGCTACGC 497
                                                                                                                                                                                                GACCACCCGCTACGCCGTCATCATCGGCGGCGCCAACTTCGGCTGCGGCTCCTCCGCGA
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                                                                                                                                                                                                                                                CGCCTTCGTCGGCCTCCCCACCGGGCCTACCCGACGCCGTTCGTCGCCCCCGGCGAGGA 431
CGTCATGATCAACCACACCACCGGCAAGCAGTACAAGCTGAAGCCTATCGGCGATGCCGG
                                                                                              GCGCATCTTCCTTCCGCAACTCCGTGGCCCACCGGTGAGGTCTACCCGTTGGAGCTAGCGGA
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APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZ
FILE REFERENCE: BB-1126
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: US/09/173,300
CURRENT FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOCTWARE: Microsoft Word Version 7.0A
SEQ ID NO 50
LENGTH: 1107
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; ORGANISM: Glycine
US-09-173-300-50
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Best Local Similarity 68.7%;
Matches 430; Conservative
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                                                                                                                                                                     AACTICGGTTGCGGCTCCTCCGGGGGGGAGCACGCCCGGTCGCGCCTGGGGGGCCTCCGGCGCC
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                                                     Score 291.2; DB 4;
Pred. No. 1.8e-57;
1; Mismatches 189;
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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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US-09-103-840A-2/c
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Best Local Similarity
Matches 215; Conserv
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3927081 TGCCGCCCTTGCCGCCTGCACCGCCGGCGCCCCGGAGCCGTTGGTGCCGCCCACACCGC 3927022
                                                                                   3927141 CGCCACCGCGAAACCAGCACCGGTGGGGTTGTCCGCGGCGGGACCCGCGGCACCTCCGG 3927082
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                                       GCACGCGCCGTCGCGTTGGGGCCCCTGGCGCACGCGCCATTGTTGCSGAGGGCTACGC 497
                                                                                                                        GTCCTCCCGCTACGCCATCATTGTCGGCGGAGCCAACTTCGGGTGCGGTTCCTCTCGCGA 437
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                                                                                                                                                                   CGCCGGTACCGGTCGCCCGCCGGCCGCCGGCGCGCGCCACCTGTGCCGCCGG 3927142
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milarity 44.8%;
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RESULT 6
US-08-984-919A-10
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                                                                                                                                                                                                                                                            RESULT 7
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                                                                                                                                                              Sequence 12, Application US/08984919A Patent No. 6383774
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: HW-2-0 TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272 TELEFAX: 970/484-9505
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SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: Chandrashekar, Ramaswamy APPLICANT: Mehta, Kapil TITLE OF INVENTION: PARASITIC NEMATITIE OF INVENTION: PROTEINS, NUCLE
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LOCATION:
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1825 Sharp Point Drive
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      PARASITIC NEMATODE TRANSGLUTAMINASE PROTEINS, NUCLEIC ACID MOLECULES,
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Pred. No.
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US-08-781-420-10
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REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HM-2-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1466 nucleotides
TENER: 1215 and 3
                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08781420 Patent No. 6248872
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Best Local S
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APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Mehta, Kapil
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TOPOLOGY: line
MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
                                                                                                                                                     TITLE OF INVENTION: Parasitic Nematode Tranglutaminase TITLE OF INVENTION: Proteins, Nucleic Acid Molecules and TITLE OF INVENTION: Uses Thereof NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
                                                   STREET: 1825 CITY: Fort Collins
CTATE: Colorado
TCA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                       ADDRESSEE: Carol Talkington Verser, ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive
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0.00035;
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US-08-781-420-12/c
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SEQUENCE CHARACTERISTICS:
FRIGTH: 1472 nucleotides
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Best Local
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,420
FILING DATE: December 3, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Chandrashekar, Ramaswamy

APPLICANT: Mehta, Kapil

TITLE OF INVENTION: Parasitic Nematode Tranglutaminase

TITLE OF INVENTION: Proteins, Nucleic Acid Molecules at

TITLE OF INVENTION: Uses Thereof
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OPERATING SYSTEM: Windows 90
SOFTWARE: Worderfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
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NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/781,420 FILING DATE: December 3, 1996
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                                                                                                                                                                                                                                COUNTRY:
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TELEFAX: 970/484-9505 INFORMATION FOR SEQ ID NO:

970/484-9505

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REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272

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Patent No. 6309644
GENERAL INFORMATION:
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Best Local
                                                                                           TELEFAX: 970/484-9505 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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LENGTH: 1472 nucleotic
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TITLE OF INVENTION:
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                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ramaswamy Chandrashekar
APPLICANT: Kapil Mehta
                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95 SOFTWARE: Worderfect for Windows, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
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                                                                           SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/874,102 FILING DATE: 12-JUN-1997 CLASSIFICATION: 424
                                                                                             TELEPHONE: 9/0/1-9505
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                                STRANDEDNESS:
                                                           ENGTH:
                                              nucleic acid
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; LOCATION:
US-08-874-102-10
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US-08-874-102-12/c
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Best Local S
Matches 81
Вb
                                                                                                        US-08-874-102-12
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                                                    Matches
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                                                                            Query Match
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NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/494-9505
                                                                                                                                                                                                   TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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TITLE OF INVENTION: PAI
TITLE OF INVENTION: PRO
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows 9 SOSTWARE: Wordperfect for Windows, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: S
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                                                                                                                       MOLECULE TYPE:
                      APPLICATION NUMBER: US/08/874,102
FILING DATE: 12-JUN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                  Local Similarity
                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 80525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Carol Talkingcon ADDRESSEE: Heska Corporation
                                                                                                                                    TOPOLOGY:
                                                                                                                                                                         LENGTH:
                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colorado
                                                                                                                                                                          1472 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ramaswamy Chandrashekar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
2..1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carol Talkington Verser, Ph.D
                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARASITIC NEMATODE TRANSGLUTAMINASE PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
                                                                  5.5%;
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Pred. No. 0.00035;
0; Mismatches 40
                                                                                                                                                                                                                                                          HW-2-C1
                                                                  Score 57; DB 4;
Pred. No. 0.0003
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                   Version
                                                                  0.00035;
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                                                        Gaps
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US-09-006-595A-10
Sequence 10, Application US/09006595A; Patent NO. 6414115; GENERAL INFORMATION:
                                                                                                                                                                                                                                    ; SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-09-006-595A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: HW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1033 A 1033
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Local Similarity 66.9%;
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Mehta, Kapil
Mehta, Kapil
TITLE OF INVENTION: Parasitic Nematode Tranglutaminase
Proteins, Nucleic Acid Molecules and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/781,420
FILING DATE: December 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                        TTTTGTTTACCTTATGTTACTGTTATTGTATTACTATTTTGCCCCTTGTTTTTAAAT 1410
                        81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/006,595A FILING DATE: 13-Jan-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1472 nucleotides
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                                                                                                                                                                     Score 57; DB 4;
Pred. No. 0.00035;
0; Mismatches 40
                                                                                                                                                                                                          DB 4; Length 1472;
                                                                                                                                                                       40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-006-595A-12
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US-09-006-595A-12/c
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                    RESULT 14
US-08-984-919A-46
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Sequence 46, Application US/08984919A
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 970/484-9505
TELEPAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1472 nucleotides
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                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,595A
FILING DATE: 13-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/781,420
FILING DATE: December 3, 1996
ATTORNEY/AGENT INFORMATION:
APPLICATION DATE: December 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                 122 TITTGTTTACCTTATGTTACTGTTATTGTATTACTATTTTGCCCCTTGTTTTTAAAT 63
                                                                                                                                                                         2 A 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: HW-2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chandrashekar, Ramaswamy
Mehta, Kapil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Carol Talkington Verser, Ph.D.
Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Pred. No. 0.00035;
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Query Match Best Local Matches

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US-08-984-919A-48/c
Sequence 48, Application US/08984919A
Patent No. 6383774
GENERAL INFORMATION:
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; LOCATION: 24..1508
US-08-984-919A-46
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                                                                                                                                                                                                     RESULT 15
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Best Local Similarity 66.9%;
Matches 81; Conservative
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GENERAL INFORMATION:
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NAME: Verser, Carol Talkington
REGISTRATION UNMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEPHAX: 970/484-9505
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INFORMATION FOR SEQ ID NO: 46:
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OPERATING SYSTEM: Windows 9
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                 TITLE OF INVENTION: PARASITIC NEMATODE TRANSGLUTAMINASE TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, TITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                               1033 A 1033
                                                                                                                                                                                                                                                                                                                                                                                                          1754 TTTTGTTTACCTTATGTTACTGTTATTGTATTACTATTTTGCCCCTTGTTTTTTAAAT 1813
                                                                                        APPLICANT: Chandrashekar, Ramaswamy APPLICANT: Mehta, Kapil
                                                                                                                                                                                                                                                            1874 A 1874
                                                                                                                                                                                                                                                                                                                                   FEATURE:
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LENGTH: 1875 nucleotides
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TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/984,919A FILING DATE: 04-DEC-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Pred. No. 0.00037;
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-984-919A-48
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INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: HW-2-CTELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1875 nucleotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/01
FILING DATE: 04-DEC-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                 1033 A 1033
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                                                                                   913 TITTITITIGITACIAGTACTIGIACAATIGIACICCIGCCIGCIACIGITCCITAICIGI 972
                                                                                                                                     122 TTTTGTTTACCTTATGTTACTGTTGTTATTGTATTACTATTTTGCCCCTTGTTTTTTAAAT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
                                                                     Match 5.5%;
Local Similarity 66.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
2 A 2
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                                                                                                                                                                                                        Score 57; DB 4; Length 1875; Pred. No. 0.00037; Mismatches 40; Indels
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Search completed: April 3, 2003, 04:39:51
Job time: 1467 secs

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Maximum
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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seq length: 2000000000
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1266
1 MAAALSGTAVSTAAL
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1: //SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: *
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: *
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: *
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT: *
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT: *
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT: *
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7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: *
8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: *
9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: *
10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT: *
11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT: *
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12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT: *
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19: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	-		6 710.5 50	-	-		No. Score Mat	
51.4 253			5.1 251				Query Match Length DB	
23 ABB92729	21 AAG4250		21 AAG42502			21 AAY28439	OB ID	
9 Herbicidally activ	P				LeuD		Description	

2 8.8 889 23	12 8.8 417 21	.5 9.0 160 22	.5 9.1 780 22	9.1 780 20	.5 9.4 139 23	20 9.3	200 22	125 9.9 639 21	5.5 9.9 869 21	5.5 9.9 639 21	9.9 557 22	5.5 9.9 553 22	.0 868	10.0 639 21	10.1 902 22	10.3 943	10.6 197 22	10.6 197 22	11.9 200 22	12.1 201 22	12.2 190 22	5 12.3 201 22	12.8 164 18	5 13.0 644 22	6 13.1 189 23	13.8 193 23	4 14.5 212 22 AAU	5 15.1 191 23	15.1 191 15 AARS	2 16.0 163 21 AABJ	5 16.3 163 22	.5 20.4 164 22 AABS	49.5 256 23 ABBS	27 49.5 256 23 ABB920	.5 50.9 256
889	417	160	780	780	139			653	869	639	557	553	868	639	902	943	197	197	200	201	190	201	164	544	189	193	212	191	191	163	163	164	256	256	256
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ABB57134	AAB58362	AAG81975	AAB84333	AAW98947	ABP32235	AAUSOUSS	12COSS	AAY74438	AAY93285	AAY74439	AAB79519	AAB79520	AAY93301	AAY74440	ABB61080	AAG91445	AAB79772	AAG91199	AAU35572	AAU34427	AAU36564	AAU38423	AAW28261	AAU34234	ABP39041	ABB48173	AAU36307	ABB54553 ·	AAR54217	AAB15395		AAB96359	ABB92092	ABB92090	920
ischae	und cancer as	۳.	Amino acid sequenc	Mitochondrial acon	Human isomerase-li	-		DT ia	Amino acid sequenc	Neisseria meningit	Q.	Corynebacterium gl		Neisseria meningit	rosophila	C glutamicum prote	orynebacter:		emophilus influ	E. coli cellular p		nella			coccus ep	nocyto	aeruq	atococa	ຜ	the	tive 3-isopro	15	11 y	idally act	Herbicidally activ

ALIGNMENTS

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Corn leuD subunit of 3-isopropylmalate dehydratase amino acid sequence

3-isopropylmalate dehydratase. Corn; soybean; wheat; rice; dihydroxyacid dehydratase; leuC; leuD; branched chain amino acid transferase; biosynthetic enzyme; antibody;

Zea mays.

W09921880-A2

06-MAY-1999.

20-OCT-1998; 98WO-US22081

28-OCT-1997; 97US-0063423.

(DUPO) DU PONT DE NEMOURS & CO

Falco SC, Cahoon RE, Hitz WD, Kinney AJ, Rafalski JA;

N-PSDB; AAX89462. WPI; 2000-022904/02

Nucleic acid fragments encoding branched chain amino acid biosynthetic enzymes $\,\,$

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RESULT 2
AAY28442
ID 2842
XX AAY2
AC AAY2
XX DT 15-F
XX Corn
KW Corn
KW bran
KW 3-is
XX 3-is
XX W099
XX W099
XX W099
XX O6-M
XX D6-M
XX D7-O
X
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                             Falco SC,
                                                                                                                                                                                                                                                                                                                                                                  Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                    3-isopropylmalate
                                                                                                                                                                                                                                                                                                                                                                                                                                               Corn; soybean; wheat; rice; dihydroxyacid dehydratase; leuC; leuD; branched chain amino acid transferase; biosynthetic enzyme; antibo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuD subunit of 3-isopropylmalate dehydratase amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMIASKAAA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LELTDVGAMKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGDAGPVIEAGGIFAYARKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPSSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFV
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249; Conserv
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                             Cahoon RE, Hitz WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 AA;
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                                                                                                                                          97us-0063423
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                          Kinney AJ,
                             Rafalski JA;
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RESULT 3
AAY28440
ID AAY2
XX AAY2
AC AAY2
XX
DE Rice
XX
COrn
KW bran
KW 3-is
XX
Oryz
XX
OS
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PD 06-M
XX
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY28439-Y28442 are fragments of corn, soybean, wheat and rice leub subunit of 3-Isopropylmalate dehydratase, amino acid sequences. Sequences AAX89442-X89465 are nucleic acid fragments that encode all or a substantial portion of dihydroxyacid dehydratase, a branched chain amino acid transferase, a leuc or a leub subunit of 3-Isopropylmalate dehydratase from wheat, corn, soybean or rice. These enzymes are involved in biosynthesis and utilization of branched-chain amino acids. The nucleic acid sequences can be used to alter the level of expression of a branched chain amino acid biosynthetic enzyme in a host cell. They can amino acid biosynthetic enzyme, and to identify inhibitors of a branched chain amino acid biosynthetic enzyme. The encoded proteins may be used to prepare antibodies for detecting the proteins in situ in cells, or in vitro in cell extracts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 200
N-PSDB;
 28-OCT-1997;
                                                                06-MAY-1999
                                                                                                  WO9921880-A2
                                                                                                                                                              3-isopropylmalate dehydratase
                                                                                                                                                                                                                             Rice leuD subunit of 3-isopropylmalate dehydratase amino acid sequence.
                                                                                                                                                                                                                                                                15-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Fig 7; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid fragments encoding branched chain enzymes \dot{\phantom{a}}
                               20-OCT-1998;
                                                                                                                                Oryza sativa
                                                                                                                                                                             Corn; soybean; wheat; rice; dihydroxyacid dehydratase; leuC; branched chain amino acid transferase; biosynthetic enzyme; a
                                                                                                                                                                                                                                                                                                                                 AAY28440 standard; Protein; 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 A 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                249 A 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AVSTAALLAPIRAPTSAFIRRSQLTCHRLHSLKCRRAGSIVPAAAAAAAGSSSPSSAVFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVSTAALLAPIRAPTSAFIRRSQLTCHRLHSLKCRRAGSIVPAAAAAAAAGSSSPSSAVFH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-022904/02
DB; AAX89465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVGTGEVYPLELTDVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFVAPGEESSR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                 98WO-US22081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1226;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
1.6e-115;
nes 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244;
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RESULT 4
AAY2841
ID AAYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid transferase, a leuC or a leuD subunit of 3-isopropylmalate dehydratase from wheat, corn, soybean or rice. These enzymes are involved in biosynthesis and utilization of branched-chain amino acids. The nucleic acid sequences can be used to alter the level of expression of a branched chain amino acid biosynthetic enzyme in a host cell. They can also be used to obtain a nucleic acid fragment encoding a branched chain amino acid biosynthetic enzyme, and to identify inhibitors of a branched chain amino acid biosynthetic enzyme. The encoded proteins may be used to prepare antibodies for detecting the proteins in situ in cells, or in
                                                                                                                                           Corn; soybean; wheat; rice; dihydroxyacid dehydratase; leuC; leuD; branched chain amino acid transferase; biosynthetic enzyme; antibody; 3-isopropylmalate dehydratase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY28439-Y28442 are fragments of corn, soybean, wheat and rice leuD subunit of 3-1sopropylmalate dehydratase, amino acid sequences. Sequences AAX89442-X89465 are nucleic acid fragments that encode all or substantial portion of dihydroxyacid dehydratase, a branched chain amino
                                                                                      Glycine max
   Misc-difference
                                                                                                                                                                                                                                                                      LeuD subunit of 3-isopropylmalate dehydratase amino acid sequence
                                                                                                                                                                                                                                                                                                                                        15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY28441 standard; Protein; 263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vitro in cell extracts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid fragments encoding branched chain amino acid biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DUPO) DU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GIFAYARKTGMIASKSA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAAALSGTAVSTA-----ALLAPIRAPTSAFIRRSQLTCHRLHSLKC---RRAGSIVPA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIFAYARKTGMIASKAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||||||||||||||||:
TAAYPTPFVAPGEETTRYAVIIGGANFGCGSSREHAPVALGAAGARAVVAEGYARIFFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAAGSSSPSSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAAAAAAPALSLAEAAPVTAVLAPCPTPSRTFRRRSWVAAICRPALKCHHSRPLTAVVAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVATGEVYPLELTDVGAWKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGDAGPVIEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAAYPTPFVAPGEESSRYAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAAAGDSTSAGVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFVGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257
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                             Location/Qualifiers
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77.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 994.5; DB 2
Pred. No. 4.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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17-OCT-2000

(first entry)

AAG26403;

AAG26403 standard;

Protein;

251 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY28439-Y28442 are fragments of corn, soybean, wheat and rice leub subunit of 3-isopropylmalate dehydratase, amino acid sequences. Sequences AAX89442-X89465 are nucleic acid fragments that encode all or a substantial portion of dihydroxyacid dehydratase, a branched chain amino acid transferase, a leuC or a leub subunit of 3-isopropylmalate dehydratase from wheat, corn, soybean or rice. These enzymes are involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid fragments encoding branched chain amino acid biosynthetic enzymes \dot{\phantom{a}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX89464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Falco
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                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1999
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                          237
                                                                                 177
                                                                                                            135
254
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                                                                                                                                                                    77
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                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                     8 TAVSTAALLAPIRAPTSAFIRRSQLTCHRL------HSLKCRRAGSIVPAAAAAA 56
ARKTGMIPSR 263
                                                                                                                                                                2000-022904/02
                                                                   EVYPLELTDVGAWKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGDAGPVIEAGGIFAY 236
                                                                                                            TRFIEPGEIKTKYAIVIGGANFGCGSSREHAPVALGASGAAAVVAESYARIFFRNSVATG
                                                                                                                            TPFVAPGEESSRYAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATG
                        ARKTGMIASK 246
                                                       EVYPLE-SEGRLCEECTTGDVVTIELGESRLINHTTGKEYRLKPIGDAGPVIEAGGIFAY
                                                                                                                                                                                                                           TRESSAATVLP----RNLAFTKLSLSHSHTLLPRFLSFPTPKSSNPRNRVAVSLQTPRAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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                                                                                                                                                                                                                                                                                Similarity 62.8
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 7; 102pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cahoon RE,
                                                                                                                                                                                                                                                                                                                                         263 AA;
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/note= "encoded
                                                                                                                                                                                                                                                                                              58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hitz WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                               Score 740.5; DB Pred. No. 2e-66; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bу
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                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                52;
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                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                              263;
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21-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 30-APR-1999; 30-APR-1999; 06-MAY-1999; 06-MAY-1999; 06-MAY-1999; 11-MAY-1999; 11-MA	Arabidopsis the Protein idential hybridisation a termination see Arabidopsis the EP1033405-A2. 06-SEP-2000. 25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 23-MAR-1999; 23-MAR-1999; 16-APR-1999; 16-APR-1999; 16-APR-1999; 16-APR-1999; 16-APR-1999;
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                                                                                                    Score 710.5; DB 21;
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7; Mismatches 62;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying target proteins (ABB90790-ABB94016) for harbickdally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are fully active identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from non-plant from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; SEQ ID NO 1302; 261pp + Sequence Listing; English.
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Best Local :
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                The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                         Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                               The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are the polypeptides or nucleic acids encoding them are the polypeptides or nucleic acids encoding them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  АВВ92089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB92089 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ANSVFINHTSGKEYKLKPIGDAGPVIEAGGIFAYARKTGMIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFVAPGEESSRYAIIVGGANFGCGS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAFIR-RSQLTCHRLHSLKCRRAGSIVPAAAAAAAGSSSPSSAVFHGECFVVGDNIDTDQ 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEDGSSLLINHTTRKEYKLKPLGDAGPVIDAGGIFAYARKAGMIPS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGAWKECKTGDVVTVDL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPFLQLKSASTIFNYKPLTSSSATIITRVAASSSDSGESITRETFHGLCFYLKDNIDTDQ
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                                                                                                                                                              as
                                                                                                                                                        herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weidler
                                                                                                              256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant; agriculture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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Score 644.5; DB 23; Pred. No. 1e-56; 27; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
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No. 2
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.2e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
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SSP-SSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTP 118 ALPCSSTKTSSSLATFRSP----FLRFNGSTSLIPSSISITSRGTSSPTIIPRAAASESDS Matches

Conservative

38;

Indels

12;

Gaps

6,

67 59

4 ALSGTAVSTAALLAPIRAPTSAFIRRSQLTCHRLHSLKCRRAG----SIVPAAAAAAAGS

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ABB920LF 12
ABB920
ID ABB92
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Best Local
                                                                                                                                                                                               The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; SEQ ID NO 1301; 261pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB92090 standard;
                                                                                                                   Sequence
                                                                                                                                                                         useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2001; 2001WO-EP09892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           АВВ92090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
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                            49.5%;
Score 627; DB
Pred. No. 5.9e
38; Mismatches
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DB 23;
5.9e-55;
hes 65;
                                                        Length 256;
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                                                                                                                                                                                                                                                 useful as herbicides.
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SSP-SSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAXPTP 118 : : : | : | | : | : | : |
                                                                              ALSGTAVSTAALLAPIRAPTSAFTRRSQLTCHRLHSLKCRRAG----SIVPAAAAAAAGS 59
                                                        ALPCSSTKTSSSLATFRSP---FLRFNGSTSLIPSSISITSRGTSSPTIIPRAAASESDS
                                                                                                                                 Similarity 54.2
36; Conservative
                                                                                                                                                                                                            256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant; agriculture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weidler M;
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                                                                                                                                                     49.5%;
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                                                                                                                                                     Score 627;
Pred. No. 5
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Matches
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                                                                                                                                                                                                                   The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to
                                                                                                                                                                                                                                                                                                                                                                   New nucleotide sequences isolated from proteins useful in industry – \ensuremath{\mathsf{proteins}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hyperthermophilic archaeon;
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                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 1040; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CNRS ) CNRS CENT NAT RECH SCI. (IFRE-) IFREMER INST FR RECH EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus abyssi
                                                                                                                                                           110 degrees centigrade. Note: This patent is in the same contains additional sequences as AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-126236/14.
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                                                                                                                             Sequence
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                  GECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFVAPGEESSR 128
Similarity
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                                                                 Conservative
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                                                                  26;
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                                                               Score 258.5; DB 22
Pred. No. 5.5e-18;
6; Mismatches 62;
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                                                                                                                                                                           patent family shown in AAB99
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W, Heilig
                                                                                                                                                                                                                                                                                                                                                                                        Pyrococcus abyssi encode
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AAB99132-AAB99143,
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YAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGA 188

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189 WKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGD-AGPVIEAGGIFAYARK 239

--IIVAGENFGCGSSREHAPLAIKAAGVSCVIAKSFARIFYRNAINIG--LPI-LEAPQA 108

Job time : 38

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match 16.3%; Score 206.5; Best Local Similarity 34.1%; Pred. No. 9.96 Matches 60; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 10 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Pages 768-769; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Forterre P, Thierry JC, Prieur D, Dietrich J, Querellou J, Weissenbach J, Saurin W, Heilig R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleotide sequences isolated from Pyrococcus abyssi encode \operatorname{proteins} useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-126236/14
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---DELEDGDVITVNWETGEV--RKNGQTLQFEPLPGFLLEIVREGGILEFIRRRG 158
                                                                   GAWKECKTGDVVTVDLANSVFINHTSGKEYKLKPI-GDAGPVIEAGGIFAYARKTG 241
                                                                                                                                                                                                                                                                 GRVWKFWDNVSTDEITPGRYNLTKDP-----QELARIAFIEVRPEFA------EKV 49
                                                                                                                                                                                                                                                                                                                                 GECFVVGDNIDTDQIIPAEH-LTLVPSKPDEYRKLGSFAFAGL-PSAAYPTPFVAPGEES 126
                                                                                                                                    RRGDVVVGGKNFGIGSSRESAALALKAAGVSGIIAKSFGRIFYRNAVNLG-~IPLLIGDT 107
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APPLICANT: Hitz, William D.

APPLICANT: Kinney, Anthony J.

APPLICANT: Kinney, Anthony J.

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Rafalski, J. Antoni

TITLE OF INVENTION BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZ

FILE REFERENCE: BB-1126

CURRENT APPLICATION NUMBER: US/09/173,300

CURRENT APPLICATION NUMBER: 60/063,423

EARLIER APPLICATION NUMBER: 60/063,423

EARLIER APPLICATION NUMBER: 097 October 28

NUMBER OF SEQ ID NOS: 54

SOFTWARE: Microsoft Word Version 7.0A

SOFTWARE: Microsoft Word Version 7.0A

TYPE: PRT

ORGANISM: Triticum aestivum

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                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC
FILE REFERENCE: BB-1126
FILE REFERENCE: BB-1126
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Query Match
                                                                                                        CURRENT APPLICATION NUMBER: US/09/173,300 CURRENT FILING DATE: 1998-10-15 EARLIER APPLICATION NUMBER: 60/063,423 EARLIER FILING DATE: 1997 October 28 NUMBER OF SEQ ID NOS: 54 SOFTWARE: Microsoft Word Version 7.0A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09173300
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   78.6%;
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Pred. No. 1.8e-133;
0; Mismatches 1;
   Score
   994.5;
   DВ
   4:
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   Length
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US-09-173-300-51
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; LOCATION: (4)
US-09-173-300-51
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                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 51
LENGTH: 263
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 157; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC
FILE REFERENCE: BB-1126
CURRENT APPLICATION NUMBER: US/09/173,300
CURRENT FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 60/063,423
EARLIER FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
NUMBER OF SEQ ID NOS: 54
NUMBER OF SEQ ID NOS: 54
                                                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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             237
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                                                                                                                                        77
                                                                                                                                                                                      20 TRFSSAATVLP---RNLAFTKLSLSHSHTLLPRFLSFPTPKSSNPRNRVAVSLQTPRAQS
                                                                                                                                                                                                               8 TAVSTAALLAPIRAPTSAFIRRSQLTCHRL------HSLKCRRAGSIVPAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIFAYARKTGMIASKAA 248
                                                                                     TPFVAPGEESSRYAIIVGGANFGCGSSSREHAPVALGAAGARAIVAEGYARIFFRNSVATG
                                                                                                                                      ARKTGMIASK 246
                                     EVYPLE-SEGRLCEECTTGDVVTIELGESRLINHTTGKEYRLKPIGDAGPVIEAGGIFAY
                                                  EVYPLELTDVGAWKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGDAGPVIEAGGIFAY 236
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                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                         24; Mismatches
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                                                                                                                                                                                                                                                   Score 740.5; DB 4
Pred. No. 2.5e-77;
                                                                                                                                                                                                                                                                   DB 4;
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                                                                                                                                                                                                                                                                     263;
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RESULT 6
US-09-134-001C-3886
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TELEX: 978450 (WUT)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENCTH: 191 amino acids
TYPE: amino acid
  GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                            Sequence 3886, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application Patent No. 5643779
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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FILE REFERENCE: GTC-007
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APPLICANT: I
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Godon, Jean-Jacques
APPLICANT: Renault, Pierre
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
TITLE OF INVENTION: synthase from Lactococcus and its applications
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (716) 263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                  170 LDDIGITLQYEEAISAYEQK 189
                                                                                                                                                                                                                                                                         222 -GDAGPVIE-AGGIFAYARK 239
                                                                                                                                                                                                                                                                                                                     116 LLPIKQPREVLNQLTKLSSQEE-----ITIDLPHQLIITSLGDFHFEIDPIWKDKLING 169
                                                                                                                                                                                                                                                                                                                                                            178 VYPL-----ELTDVGAWKECKTGDVVTVDLANSVFINHTSGKEYKLKPI------
                                                                                                                                                                                                                                                                                                                                                                                                                            118 PFVAPGEESSRYAIIVGGANFGCGSSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release ""
                                                                                                                                                                                                                                                                                                                                                                                                        57 DFILNAPKYKKASLLISGDNFGSGSSREHAAWALSDYGFRAIIAGSYSDIFYNNALKNG- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GSSSPSSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 58; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Application US/08403866 5643779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.1%; Score 191.5; DB 1; 29.0%; Pred. No. 4.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
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; MOLECULE TYPE: US-08-887-798-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08887798 Patent No. 5922556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3886
LENGTH: 189
TYPE: PRT
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                                                                                     TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 110
STREET: New York
CITY: New York
STATE: New York
TOWNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mayeux, Richard
APPLICANT: Graziano, Josep
APPLICANT: Freyer, Greg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PARKINSON'S DISEASE TESTS NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 VGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGAMKE- 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129
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                                        TOPOLOGY:
                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
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                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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                                                      amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.1%; Score 166; DB 4; Length 189; 38.5%; Pred. No. 3.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Joseph H.
                                                                                                                                                                                                                                                                                                       US/08/887,798
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Mismatches
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Query Match Best Local Similarity

9.1%;

Score 115.5; DB 2; Pred. No. 0.00022;

Length 780;

Gaps

12;

120

154

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; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5208
; LENGTH: 914
; TYPB: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5208
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                                                                                                                                                                                                                                                                     US-09-355-115-7
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                        Sequence 7, Application US/09355115
Patent No. 6200788
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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
APPLICANT: TERRIL Stefano R.
APPLICANT: TOGURI, Toshihiro
APPLICANT: TOGURI, Toshihiro
APPLICANT: TOGURI, Toshihiro
TITLE OF INVENTION: BETA-KETOACYL-ACP SYNTHETASE II ENZYMES AND GENES
TITLE OF INVENTION: CODING FOR SAME
FILE REFERENCE: 049441/0121
CURRENT APPLICATION NUMBER: US/09/355,115
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: PCT/JP98/00194
EARLIER FILING DATE: 1998-01-20
EARLIER APPLICATION NUMBER: JP 9-011430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          656 RWYVIGDENYGEGSSREHAALEPRHLGGRAIITKSFARIHETNLKKQG-LLPLTFADPAD 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          611 DNISNNLLIGA--INIENGKANSVRNAVTQEFGPVP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDNIDTDQIIPA-----EHLTLVPS-----KPDEYRKLGSFAFAGLPS 112
                                                                                                                                                                                                                                                                                                                                                  VNVTAKKE 876
                                                                                                                                                                                                                                                                                                                                                                                        INHTSGKE 215
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o. 6380370
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23.9%;
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US-08-858-207A-388
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NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
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Best Local S
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                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/858,207A
FILLING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION NUMBER: 60/017670
FILLING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glimmi, Edward R
NAME: Glimmi, Edward R
NAME: Glimmi, Edward R
NAME: Glimmi, Edward R
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TYPE: PRT
ORGANISM: Barley
                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19400 U.L. FORM:
COMPUTER READABLE FORM:
COMPUTER TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                      REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 LASVFGSDVDTFYDRLLAGES------GVGPIDRFDASSFPTRFAGQIRGFS 102
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                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM CON OPERATING SYSTEM:
                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GARAIVAEGYARI--FFRNSVATGEVYPLELTDVGAW------KECKTGDVVTV 200
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Knowles, David
                                   610-270-5090
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                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
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;; TYPE: amino acid; STRANDEDNESS: Single; TOPOLOGY: linear; MOLECULE TYPE: NO. 6348328e US-08-858-207A-388
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                                                                                                            Qy
                                                                                                                                                                                                                                                 ; TOPOLOGY: unknown ; MOLECULE TYPE: peptide US-08-804-227C-8
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US-08-804-227C-8
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Best Local S
Matches 31
                                                                                                                                                       Query Match 6.8%; Score 85.5; DB 2; Best Local Similarity 23.8%; Pred. No. 9.6; Matches 64; Conservative 27; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08804227C Patent No. 5876991
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4550 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMM Compatible
OPERATING SYSTEM: MS-DOS
SOSTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION UNMBER: 35,784
REGISTRATION UNMBER: X-8231
REFERENCE/DOCKET NUMBER: X-8231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: DeHOff, Bradley S.
APPLICANT: CHISTOSS, Stuart A.
APPLICANT: KINSTOSS, STUART A.
APPLICANT: ROSTECK, Paul R., Jr.
APPLICANT: SUTTON, FOLIXETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 VTVDLANSVFIN------HTSGKEYKLKPIGDAGPVIEAGGIFAYARK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 GSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGE---VYPLELTDVGAWKECKTGDV 197
                                                              273 REGQEAVLRAACAQARVDPAEVRFVELHGTGTPVGDPVEAHALGAVHGSGRPADDPLLVG 332
61 VTVDLEQQKIISPVEEFTFEIDSKWKHKLLNSLDDIGITLQYEELIAAYEK 111
                                                                                                          44 RAGSIVPAAAAAAGSSSPSSAVF---HGECFVVGDNIDTDQI-----IPAEHLTLVP 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.9%; Score 87; DB 4; Length 119; Local Similarity 27.9%; Pred. No. 0.025; es 31; Conservative 16; Mismatches 50; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GSSRDHAAWALADYGFKVVIAGSFGDIHYNNELNNGMLPIVQPREVREKLA--QLKPTDQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                       91;
                                                                                                                                                                                                   Length 4550;
                                                                                                                                                          Indels 87;
                                                                                                                                                     Gaps
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	446	393 LAPGGAPLLAGVSSFGIGGTNCHVVLEHLPSRPTPAVSVAASLPDVPPLLLSAR 4	Дb
	159	121 -APGEESSRYAIIVGGANFGCGSSREHAPVALGAAGARAI	Qγ
	392 .	333 SVKTNIGHLEGAAGIAGLVKAALCLRERTLPGSLNFATPSPAIPLDQLRLKVQTAAAELP	Дb
	120	94 SKPDEYRKL-GSFAFAGLPSAAYPTPFV	Qy
	332	273 REGGEAVLRAACAQARVDPAEVRFVELHGTGTPVGDPVEAHALGAVHGSGRPADDPLLVG	Db 43
13	sd.	6.8%; Score 85.5; DB 2; Length 4550; Best Local Similarity 23.8%; Pred. No. 9.6; Matches 64; Conservative 27; Mismatches 91; Indels 87; Ga	?
		TIPE: duling delig TOPOLOGY: unknown MOLECULE TYPE: peptide -08-804-198-2	us;
		ON FOR SEQ E CHARACTER H: 4550 am	
		Z Z Z	
		K B	
		G.	
		DATA:	
		SYSTEM: Macintos	
		MEDIUM TYPE: Floppy disk COMPUTER: Marintosh	, .
		46285	
		STATE: IN	
		CO.	
		: Richardson, Mark A. : Rosteck, Paul R., Jr.	
		APPLICANI: Bulyett, Stuart A. APPLICANI: Kuhstoss, Stuart A. APPLICANI: Rao, Nagaraja R.	
		A5320 RMATION:	
		SULT 12 -08-804-198-2 Sequence 2, Appli	RE US
		490 PCGGRGELVAALGGFAAGRVS	ДD
		220 PIGDAGPVIEAGGIFAYARKTGM	Qy
	489	447 -SEGALRAQAVRLGEYVERVGADPRDVAYSLASTRTLFEHRAVV	ם
	219	160 VAEGYARIFFRNSVATGEVYPLELTDVGAWKECKTGDVVTVDLANSVFINHTSGKEYKLK	Qy
	446	393 LAPGGAPILAGYSSEGIGGTNCHVYLEHLPSRPTPAVSVAASLPDVPPLLLSAR	망성
	150	333 SVKINIGHLEGAAGIAGLVKAALCLKERTLEGSLNEATESPALPLUQLRLKVQTAAAELP	5 5

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US-08-791-115B-5
                                  RESULT 14
US-09-413-814-46
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Patent No. 626224
Sequence 46, Appli
Patent No. 6225064
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yung, W.K. Alfred
APPLICANT: Tavtigian, Sean V.
TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/791,115B FILING DATE: 30-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-683-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 PIGDAGPVIEAGGIFAYARKTGMIASKAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 VAEGYARIFFRNSVATGEVYPLELTDVGAWKECKTGDVVTVDLANSVFINHTSGKEYKLK 219
                                                                                                                                              132 IVGGANFGCGSSREHAPVALGAAGARAIVAE 162
                                                                                                                                                                                                                                                         151
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 38,957
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
ZIP: 22204
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                                                                                                                                                                                                                 VVGDNIDTDQIIPAEHLTLVPSKPDEYRKL-GSFAFAGLPSAAYPTPFVAPGEESSRYAI 131
                                                                                                                                                                                                                                                       REPAEARRRR-----RRHLPLLERGGEAAAAAAAAAAAPGRGSESPVTISRAGNAGEL- 203
                                                                                                                                                                                                                                                                                          RAPTSAFIRRSQLTCHRLHSLKCRRAGSIVPAAAAAAA----GSSSP---SSAVFHGECF 72
                                                                                                            --GGSRSEDYSSSPHS----AAAAARPLAAE 271
                                                                                                                                                                                                                                                                                                                                49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                   Application US/09413814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             742 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                 -VSPLLLPPTRRRRRHIQGPGPVLNLPSAAAAPP-VARAPEAAG---
                                                                                                                                                                                                                                                                                                                                               6.6%;
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                                                                                                                                                                                                                                                                                                                                               Score 83;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                  ed. No. 1.2;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 742;
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                                                                                                                                                                                                                                                                                                                                  56; Indels
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US-08-317-310A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DAX sequences for enzymatic synthesis of polyketide TITLE OF INVENTION: heteropolyketide compounds FILE REFERENCE: PCT/US 99/23535 CURRENT APPLICATION NUMBER: US/09/413,814 CURRENT FILING DATE: 1999-10-07 EARLIER FILING DATE: 1999-10-07 EARLIER APPLICATION NUMBER: DE 198 46 493.2 EARLIER FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 585870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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APPLICANT: Cino, Paul M
APPLICANT: Cougherty, Brian A
APPLICANT: Goldberg, Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
                                                   COUNTAX.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TWONTER: TEM PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: WHITE, MOTTIS F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1152 IALHAVDEAGPTRLALRGLHAWVPQCEHVQPATIPGAGMWREGGVY-MITGG--FG---- 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1097 VTPAALALGDEATRPEWAILHG--MVAGLSRDYPE---WREVSIDGGDPSPHRCEGLARL 1151
                                                                                                                                                                                                                                                                                           APPLICANT: WHITE, MOTTIS F. APPLICANT: SUN, Xiao Jian APPLICANT: PIECE, Jacalyn H. TITLE OF INVENTION: THE IRS F. NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1254 EAMRRYFDAAHARFGAIDGILHAAG----
                SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,310A
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
mes 51; Conserv
FILING DATE:
                                                                                                                                                                                              STATE: Massachusetts
                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGAWKE----CKTGDVVTV 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beyer, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08317310A
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                                                                                                                                                                                                                                       28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --SFAFAGL----PSAAYPTPFVAPG----EESSRYAIIVGGANFGCGSS 143
  03-OCT-1994
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                                                                                                                                                                                                                                                                                                                      IRS FAMILY OF GENES
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CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: LOUIS MYETS
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 35,965
REGERENCE_DOCKET NUMBER: 35,965
REGISTRATION THEORNATION:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1234 amino acids
TOPOLOGY: 11near
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-317-310A-15

Ouery Match
FRAGMENT TYPE: internal
US-08-317-310A-15

OUERY MATCH
OUERY MATCH
Salicative 15; Mismatches 45; Indels 55; Gaps
FRAGMENT TYPE: PRESENTING THE SECOND TO THE SECOND
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Title:
Perfect score:
Sequence:
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Maximum
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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       1266
1226
994.5
740.5
740.5
184
1164.5
155.5
153.5
153.5
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155.5
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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1266
1 MAAALSGTAVSTAALLAPIR......AGGIFAYARKTGMIASKAAA 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237916 seqs, 58723674 residues
         .: //gn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
.: //gn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
.: //gn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
.: //gn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
.: //gn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
.: //gn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
.: //gn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
.: //gn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
.: //gn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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         12 US-10-027-450-47
12 US-10-027-450-53
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12 US-10-027-450-51
10 US-09-815-242-14016
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10 US-09-815-242-11162
10 US-09-815-242-11164
10 US-09-738-626-4953
9 US-09-738-626-4953
9 US-09-738-626-5199
10 US-09-738-626-711648
10 US-09-79-307-12
10 US-09-779-307-12
10 US-09-779-307-12
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Sequence 47, Appl
Sequence 53, Appl
Sequence 51, Appl
Sequence 510, Appl
Sequence 5100, Appl
Sequence 11016, A
Sequence 112157, A
Sequence 10202, A
Sequence 4953, Ap
Sequence 4953, Ap
Sequence 4953, Ap
Sequence 5199, Ap
Sequence 71648, A
Sequence 71648, A
Sequence 700, App
Sequence 7, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
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	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.2	6.2	6.2	6.3	6.4	6.4	6.4	6.4	6.5	6.6	6.6	6.7	7.0	7.0	7.1	7.3	7.5
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	US-09-903-199-5	US-09-903-216-5	US-09-903-063-5	US-09-859-604-5	US-09-903-248-5	US-09-436-184-5	US-09-976-673-18	US-09-976-673-16	US-09-738-626-6532	US-09-999-162-14	US-10-029-180-32	US-09-789-836-5	US-09-815-242-11984	US-09-344-882-30	US-09-815-242-12929	US-09-815-242-12159	US-09-749-728B-11	US-10-161-510-10	US-09-738-626-4284	US-09-825-414-70	US-09-738-626-4887	US-09-738-626-6032	US-09-738-626-4543	US-09-864-761-42633	US-09-924-396B-18	US-09-976-059-13
•	Sequence 5, Appli	Sequence 5, Appli	Ç	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 18, Appl	Sequence 16, Appl	•	Sequence 14, Appl	Sequence 32, Appl	Sequence 5, Appli	Sequence 11984, A	Sequence 30, Appl	Sequence 12929, A	Sequence 12159, A	Sequence 11, Appl	Sequence 10, Appl	Sequence 4284, Ap	Sequence 70, Appl	Sequence 4887, Ap	Sequence 6032, Ap	Sequence 4543, Ap	Sequence 42633, A	Sequence 18, Appl	Sequence 13, Appl

ALIGNMENTS

RESULT 1 US-10-027-450-47

Sequence 47, Application US/10027450 Patent No. US20020102715A1

ENZYMES

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GENERAL INFORMATION:

APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZ
FILE REFERENCE: BB-1126
CURRENT APPLICATION NUMBER: US/10/027,450
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/063,423
PRIOR FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 47
LENGTH: 249
TYPE: BRT
ORGANISM: Zea mays
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181 LELTDVGAWKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGDAGPVIEAGGIFAYARKT
                                                        121 APGEESSRYAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYP 180
                                                                                                                                          61
                                                                                                                                                           61 SPSSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFV 120
                                                                                                                                                                                                                  SPSSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFV
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                                                                                                                                                                                                                                                                                                                                      Length 249;
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                     240
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181 LELTDVGAWKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGDAGPVIEAGGIFAYARKT 240

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RESULT 3
US-10-027-49
(Sequence 49, Application US/10027450
Patent No. US20020102715A1
GENERAL INFORMATION:
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENGINEER OF SERION NUMBER: US/10/027,450
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/063,423
PRIOR FILING DATE: 1997 October 28
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SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 53
LENGTH: 224
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC FILE REFERENCE: BB-1126 CURRENT APPLICATION NUMBER: US/10/027,450 CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/063,423 PRIOR FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
                                                                                                                                                                                                                                                                                                                                                                                           249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVGTGEVYPLELTDVGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFVAPGEESSR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVSTAALLAPIRAPTSAFIRRSQLTCHRLHSLKCRRAGSIVPAAAAAAAAGSSSPSSAVFH 63
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Pred. No. 7.9e-110;
0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/10/027,450
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/063,423
PRIOR FILING DATE: 1997 October 28
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 51
LENGTH: 263
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Oryza :
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                                                                                                                                                                                Query Match
Best Local S
Matches 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Falco, Saverio Carl
APPLICANT: Hitz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC
FILE REFERENCE: BB-1126
                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 TPFVAPGEESSRYAIIVGGANEGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 SVATGEVYPLELTDVGAMKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGDAGPVIEAG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 GIFAYARKTGMIASKAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SVATGEVYPLELADTGAWKECKTGDVVTVELDNCVMINHTSGKQYKLKPIGDAGPVIEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 AAAAAAGSSSPSSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AAAAAAAGDSTSAGVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFVGLP 120
                                                                                                                 20 TRFSSAATVLP---RNLAFTKLSLSHSHTLLPRFLSFPTPKSSNPRNRVAVSLQTPRAQS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAAALSGTAVSTA-----ALLAPIRAPTSAFIRRSQLTCHRLHSLKC---RRAGSIVPA 51
                                                                                                                                    8 TAVSTAALLAPIRAPTSAFIRRSQLTCHRL------HSLKCRRAGSIVPAAAAAA 56
                                             INFORMATION:
                                                                                                                                                                              al Similarity
157; Conserv
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                                                                                                                                                                           58.5%; Score 740.5; DB 1 62.8%; Pred. No. 2.8e-63; tive 24; Mismatches 52
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77.0%; Pred. No. 1.3e-87;
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                                                                                                                                                                                                             DB 12; Length 263;
                                                                                                                                                                                52;
                                                                                                                                                                                Indels 17;
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195 177 135

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APPLICANY: Yamamoto, Robert T.
APPLICANY: Yaw, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
RESULT 6
US-09-615-242-5730
; Sequence 5730, Application
; Patent No. US20020061569A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pseudomonas aeruginosa US-09-815-242-11900
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Best Local Similarity 32.1
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 11900
LENGTH: 212
TYPE: PRT
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                     123 NG-LLPIILPEAEVDELFRQVEANEGYQLSIDLAAQT-VTRPDGK 165
                                                                                                                                                                                                                                                                                         63 LNPDFVLNQPRYQGASVLLARENFGCGSSREHAPWALDEYGFRTVIAPSYADIFFNNSFK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                           77 NIDTDQIIPAEHLTLV-----PSKPDEYRKLGSFAFAGLPSAAYPTPFVAPGEESS--- 127
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4 ARKTGMIPSR 263
                                                                                                                                                                                                                                    TGEVYPL-----ELTDVGAWKECKTGDVVTVDLANSVFINHTSGK 214
                                                                                                                                                                                                                                                                                                                                        -----RY---AIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVA 174
                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wall, Daniel
Trawick, John D.
Carr, Grant J.
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Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.5%; Score 184; DB 10; 32.1%; Pred. No. 4.2e-10; tive 23; Mismatches 45;
                                                         US/09815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 44;
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; LOCATION: (1)...(644)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-5730
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US-09-815-242-14016
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                            Sequence 14016, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5730
LENGTH: 644
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                              TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, APPLICANT: Ohlsen, K
     CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 VGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRN 171
: | |||||||||| || | | | :| :: ||: |
532 ITGDNFGCGSSREHAAWALKDYGFHIIIAGSFSDIFYMN 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 KCRRAGSIVPAAAAAAAGSSSPSSAVFHGECFV------VG 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
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Similarity 33.3%;
                                                                                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                        Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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Yamamoto, Robert T.
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Zyskind, Judith W.
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; Pred. No. 1.46
12; Mismatches
                                                                               of Essential Genes
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 14016
LENGTH: 201
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US-09-815-242-14016
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                                                                                                                                     PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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Best Local :
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                        PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Ess.
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITER.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 GSFAFAGLPSAAYPTP-FVAPGEESSRYAIIVGGANFGCGSSREHAPVALGAAGARAIVA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 RRAGSIVPAAAAAAAGSSSPSSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKL 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                 of Essential Genes
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APPLICANT: Trawlck, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-05-21
PRIOR APPLICATION NUMBER: 60/206.848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207.727
PRIOR TILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242.578
PRIOR APPLICATION NUMBER: 60/242.578
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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US-09-815-242-10020
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US-09-815-242-10020
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Best Local S
Matches 40
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Best Local (
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
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162 EGYARIFFRNSVATGEVYPLELTD 185
                                                                                           103 GSFAFAGLPSAAYPTP-FVAPGEESSRYAIIVGGANFGCGSSREHAPVALGAAGARAIVA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 VGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRN 171
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                                                                                                                                                                                                                                                                      Local Similarity
                                            45 NDWRFLD-EKGQQPNPDFVLNFPQYQGASILLARENFGCGSSREHAPWALTDYGFKVVIA 103
                                                                                                                                                                                            43 RRAGSIVPAAAAAAAGSSSPSSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKL 102
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                                                                                                                                             ITGDNFGCGSSREHAAWALKDYGFHIIIAGSFSDIFYMN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                              Conservative
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40.4%; Pred. No. 2.2e-07;
tive 10; Mismatches 41;
                                                                                                                                                                                                                                      12.1%; Score 153.5; DB 10; 30.6%; Pred. No. 3.3e-07; tive 19; Mismatches 56;
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                                                                                                                                                                                                                                                                                           Length 201;
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                                                                                                                                                                                                                                              Gaps
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEN.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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US-09-815-242-11165
                                                                                                                                                                                                                                        US-09-738-626-4953
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                  GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11165
LENGTH: 200
TYPE: PRT
                                                                                                                                                                                          Sequence 4953, Application US/09738626 Publication No. US20020197605A1
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APPLICANT:
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APPLICANT:
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       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 PSFADIFYGNSF-NNQLLPVKLSD 126
                                                                                                                                                                                                                                                                                                                                                                               158 AIVAEGYARIFFRNSVATGEVYPL----ELTDVGAWKECKTGDVVTVDL 202
                                                                                                                                                                                                                                                                                                                                 99 VMIAPSFADIFYNNSL-NNHMLPIRLSEBEVEBIFQWVMANEGKQIHVDL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 YRKLGSFAFAGLPSAAYPTP-FVAPGEESSRYAIIVGGANFGCGSSREHAPVALGAAGAR 157 : | | | | | | | | | | | | | :
                                                                                                                                                                                                                                                                                                                                                                                                                                  46 WRYLD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 AGSIVPAAAAAAAGSSSPSSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKP-----DE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 11.9%;
ocal Similarity 28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Conservative
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  TATEISHI, NAOKO
                                           HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                              ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr, Grant J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto, Robert T.
                            YOKOI, HARUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                               ----VEGTKPNPEFVLNYPQYQGATILLARKNLGCGSSREHAPWALADYGFK 98
                                                                                                                  HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 151; DB 10;
Pred. No. 5.6e-07;
N1. Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 200;
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                                                                                                                                                   APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, MASATO
ITTILE OE INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: J99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR EILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VOI: 3.0
SEQ ID NO 5199
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 4953
LENGTH: 197
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                                                                    ; ORGANISM: Corynebacterium glutamicum US-09-738-626-5199
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US-09-738-626-5199
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Query Match
Best Local Similarity
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APPLICANT:
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                       ENGTH: 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 IIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYP-LELTDVG-A 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 WK--ECKTGDVVTVDLANSVFINHTSGKEYKLKPIGDAGPVIEAGGIFAYAR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 VLVAGPDFGTGSSREHAVWALMDYGFRAVFSSRFADIFRGNSGKAGMLTGIMEQSDIELL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 NVDTDQIIPAVYLKRVTR----
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Similarity 30.2%;
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANDO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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10.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TGFEDGLFSNWRQNDPNFVLNTDTYKNGS
Score 130; DB 9;
Pred. No. 0.00046;
                      Length 943;
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Gaps

6;

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RESULT 11

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Matches

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US-09-815-242-11648
                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Klebsiella pneumoniae US-09-815-242-11648
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                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11648
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               831 TNLLGIRAVITESFERIHRSNLIGMG-VVPLQFPAGESHESLGLDGTETFDITGLTALNE 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 LP-----SAAYPTPFVAPG------EESSRY-----AIIVGGANFGCGSSREHAPVA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 -TSGKEYKLKPIGDAGPVIE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 LGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGAWKECKTGDVVTVDLANSVFINH 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       771 LQNQLVDIAGGYTRDFTQEGAPQAFIYDASVNYKAAGIPLVVLGGKEYGTGSSRDWAAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 713 LGDSVTTDHISPAS--SIKPGTPAAQYLDEHGVERHDYNSLGSRRGNHEVMMRGTFANIR 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 VGDNIDTDQIIPAEHLTLVPSKP------DEYRKLGS-----FAFAG 109
162 EGYARIFFRNSVATGEVYPLELTD 185
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                                                                                                           103
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                                                                                                                                                                                                   43
                                                                                                                                                                                                                                              Local Similarity 28.5 es 41; Conservative
                                                                                                        GSFAFAGLPSAAYPTP-FVAPGEESSRYAIIVGGANFGCGSSREHAPVALGAAGARAIVA 161
                                                             NDWRFLD-DKGQQPNPEFVLNFPEYQGASILLARENFGCGSSAS-TPWALTDYGFKVVIA 102
                                                                                                                                                                                                   RRAGSIVPAAAAAAGSSSPSSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKL 102
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Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                        9.5%;
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                                                                                                                                                                                                                                                   Score 120; DB 10;
Pred. No. 0.00052;
7; Mismatches 60;
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                                                                                                                                                                                                                                                                                           Length 200;
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US-09-925-302-700
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                                                                       ; ORGANISM: Homo sapiens US-09-779-307-2
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LENGTH: 417
TYPE: PRT
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GENERAL INFORWATION:
APPLICANT: Taupier Jr., Raymond
APPLICANT: Maiumder, Kumud
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APPLICANT: Rosen et al.
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Patent No. US2002
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                     APPLICANT: Majumder, Kumud
APPLICANT: Vernet, Corine
APPLICANT: Vernet, Corine
APPLICANT: Prayaga, Sudhirdas
TITLE OF INVENTION: Polynucleotides and Polypeptides Encoded Thereby
FILE REFERENCE: 15966-662 US
CURRENT APPLICATION NUMBER: US/09/779,307
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/180,880
PRIOR PILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 896 SOFTWARE: PatentIn Ver. 2
                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/181,656
PRIOR FILING DATE: 2000-02-10
                                                                                                                                                                                       SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                            PRIOR FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 43
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                                                                                                                       LENGTH: 538
TYPE: PRT
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les 44; Conserv
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Pred. No. 0.0082;
4; Mismatches 50;
           Score 105.5; DB 10; Pred. No. 0.048;
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	Mat Qy Db Db Db Db Db Oy	Matches 61; Conservative 19; Mismatches 97; Indels 53; Gaps 17 APIRAPTSAFIRRSQLTCHRLHSLKCRRAGSIVPAAAAAAGSSSPSSAVFHGECFVVGD 76 11
136ANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVG 187		77 N 166 S
188 AWKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGDAG : :		136 - 212 D
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Search completed: March 31, 2003, 09:13:3 Job time: 16 secs

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No. Score Match Length DB ID Description 1 710.5 56.1 251 2 H84861 2 651 51.4 253 2 T47781 3 652 49.5 256 2 A74781 3 11.5 24.6 166 2 A72363 4 311.5 24.6 166 2 A72363 6 272 21.5 161 2 E69328 6 271 21.1 168 2 D64459 7 267.5 21.1 168 2 D64459 9 266 20.5 16.3 2 B97290 9 266 20.5 16.3 2 B97290 9 26.5 19.9 162 2 E69051 12 250.5 19.9 170 2 E69210 13 24.9 19.7 165 2 H69469 14 223.5 11.0 166 2 D72394 15 227.5 18.0 166 2 F75355 18 202.5 19.9 170 2 F64458 17 206.5 16.3 16.3 2 G71180 18 202.5 16.0 16.3 2 G71180 19 192 15.2 659 2 F70453 20 191.5 15.1 191 2 T70453 21 18 14.5 21.5 2 G82564 22 18 14.5 21.5 2 G82564 23 18 14.5 21.5 2 G82564 24 18 14.1 199 2 G69650 25 17.4 5 13.8 193 2 AF133 29 172 13.6 200 2 S75839 20 174.5 13.8 193 2 AF133 3-isopropylmalate	Pred. No. score grea and is der	Database: PIR_73:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Total number of hits satisfying chosen parameters: 283224	Searched: 283224 segs, 96134422 residues	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Title: US-10-027-450-47 Perfect score: 1266 Sequence: 1 MAAALSGTAVSTAALLAPIRAGGIFAYARKTGMIASKAAA 249	Run on: March 31, 2003, 09:06:23 ; Search time 44 Seconds (without alignments) 544.033 Million cell updates/sec	OM protein - protein search, using sw model	GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
Query Match Best Local Similarity 59.5%; pred; No. 4e-51; Matches 153; Conservative 27; Mismatches 62; Indels 15; Gaps 6; Qy 1 MANALSGTAVSTAALLAPIRAPTSAFIRRSQLTCHRLHSLKCRRAGSIVPAAAAAAGSS 60	A; Molecule type: DNA A; Residues: 1-251 <sto> A; Cross-references: GB:AE002093; NID:g3763918; PIDN:AAC64298.1; GSPDB:GN00139 C; Genetics: A; Gene: At2g43090 A; Map position: 2</sto>	euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente: Nature 402, 761-768, 1999 A; Title; Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana. A; Reference number: A84420; MUID:20083487; PMID:10617197 A; Accession: H844861 A; Status: preliminary	H84861 3-isopropylmalate dehydratase, small subunit [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C; Accession: H84861 C; Accession: H84861 R; Lin, X; Kaul, S; Rounsley, S,D; Shea, T,P; Benito, M.I; Town, C.D.; Fujii, C.R; Lin, X; Kaul, S; Rounsley, S,D; Shea, T,P; Benito, M.I; Town, C.D.; Fujii, C.M. Koo, H. Moffat, K S; Cronin, T,A; Shen, M; VanAken, S,E; Umayam, L; Tallon	RESULT 1	ALIGNMENTS	154.5 12.2 201 2 C85489 isopropylmalate	155.5 12.3 201 2 AC0516 155 12.2 201 2 S07306 155 12.2 201 2 S074011 154 5 12.2 701 2 C90638	7.5 13.2 216 2 F97693 1.5 12.8 177 2 H75373 1.5 12.6 190 2 B89998 8.5 12.5 211 2 AB9561	169 13.3 213 2 C81836 168 13.3 200 2 A829071 167 5 13.3 200 2 A829070	171.5 13.5 202 2 171.5 13.5 208 2 170 13.4 213 2 169.5 13.4 193 2

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 < DAN>
A;Residues: 1-253 < CDAN>
A;Cross references: EMBL:ALI63527
A;Experimental source: cultivar Col
C;Genetics:
A;Map Position: 3
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submitted to the Protein St
A;Reference number: Z24476
A;Accession: T47781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84862
R;Lin, X:; Kaul, S:; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84682
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-256 <STO>
A;Cross-references: GB:AE002093; NID:g3763919; PIDN:AAC64299.1; GSPDB:GN00139
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A;Gene: At2g43100
A;Map position: 2
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                                                           FVAPGEESSRYAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEV 178
                                                                                                             NEALANTTFHGLCYVLKDNIDTDQIIPAGAACTFPSNQQERDEIAAHALSGLPD-FHKTR 126
                                                                                                                                SSP-SSAVFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLDSAAYPTP 118
                                                                                                                                                                                                                  ALSGTAVSTAALLAPIRAPTSAFIRRSQLTCHRLHSLKCRRAG----SIVPAAAAAAAAGS
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                                        FIEPGENRSKYSIIIGGENFGCGSSREHAPVCLGAAGAKAIVAESYARIFFRNSVATGEV
                                                                                                                                                                                      ALPCSSTKTSSSLATFRSP---FLRFNGSTSLIPSSISITSRGTSSPTIIPRAAASESDS
   YPLELTDVGAWKECKTGDVVTVDLANS--VFINHTSGKEYKLKPIGDAGPVIEAGGIFAY 236
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135; Conser
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Sequence Database, April 2000
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Pred. No. 3e-44;
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A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: A72363
A;Status: pretiminary
A;Molecule type: """
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.;
                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-166 <ARN>
A;Cross-references: GB:AE001730; GB:AE000512; NID:g4981062; PIDN:AAD35640.1; PID:g498
A;Experimental source: strain MSB8
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                                                                                                                 186 VGAWKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGD-AGPVIEAGGIFAYARK
                                                                                                                                                52 DIKGSIIVAGENFGCGSSREHAPVAIKAAGISCVIAKSFARIFFRNAINIG----LPIVE
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                                                                               Similarity
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                      24.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         small subunit - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                       Score 311.5; DB 2;
Pred. No. 1.6e-18;
""" tomatches 54;
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Archaeoglobus
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Nature 390, 304-270, 207, A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiacn, F. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, A;Title: The complete genome sequence of the hyperthermophilic, R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997 3-isopropylmalate dehydratase, small subunit (leuD-1) homolog - Archaeoglobu C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C;Accession: E69328 A;Cross-references: GB:AE001061; GB:AE000782; NID:g2689384; PIDN:AAB90610.1; A; Molecule type: DNA A; Residues: 1-161 <KLE> A; Status: preliminary; nucleic acid sequence not shown; translation A;Reference number: A69250; MUID:98049343; A;Accession: E69328 Matches Query Match 69 Local GECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGL-PSAAYPTPFVAPGEESS 127 Similarity Conservative 21.5%; 30; Score 272; DB 2; Pred. No. 2.7e-15; Mismatches Length 161 P.; sulfate-reducing Kaine, B.P.; not shown Gaps PID: g264 6; Sykes, arch

N

GRAWKFGDDIDTDVIIQGKYLVI--NEPEE---LAKHVFENLRPEFA--

-KEVK 47

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RESULT 7
D64459
3-isopropylmalate dehydratase (EC 4.2.1.33) - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul
C;Accession: D6459
C;Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE000738; NID:g2983801; PIDN:AAC07359.1; PID:g2983802; GB:AE00065
A;Experimental source: strain VF5
C:Genetics:
                                                                                                                                                                                                                                                                                                                                          R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Bla Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woes
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C;Date: 08-May-1998 #sequence_revision
C;Accession: E70421
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E70421
3-isopropylmalate dehydratase -
A;Map position: REV1223059-1222553
C;Keywords: carbon-oxygen lyase; h
                                                                                                       A;Cross-references: GB:U67568; GB:L77117; NID:g2826383;
                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-168 <BUL>
                                                                                                                                                                                                                                             A;Title: Complete genome sequence of the methanogenic archaeon, A;Reference number: A64300; MUID:96337999; PMID:8688087 A;Accession: D64459
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A; Residues: 1-219 <AQF>
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Pred. No. 4.7e
27; Mismatches
       hydro-lyase
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                                                                                                    PIDN:AAB99283.1; PID:g1591913;
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RESULT 9
B97290
3-isopropylmalate dehydratase, small chain [imported] - Clostridium acetobutylicum C; Species: CLostridium acetobutylicum C; Species: CLostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C; Accession: B97290
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Nolling, J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacteri A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, ', 'Qiu, D.; Spadafora, R.; Vicalre, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-isopropylmalate dehydratase, LeuD subunit - Methanobacterium thermoautotrophicum c;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C;Accession: E69210
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E69210
A; Experimental source: C; Genetics:
                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-163 <KUR>
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A;Experimental source: strain Delta H
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A; Residues: 1-170 < MTH>
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                                               A;Cross-references: GB:AE001437;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 IIRGRVWRFGDNVDTDMIIPGRYL-----RTFSLDELASHVMEGARPEFASQ---VRKGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVDA----DDGDEVSIDLRSGQIRNLTAGSEYRMKPFNDYMLSILEDGGLVNHYLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKGISEKVNEGDELEVNLETGEIKNLTTGEVLK-----GQKLPEFMMEILEAGGLMPYLKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESSRYATIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----IIVAGRNFGCGSSREQAPVALKHAGVVAIIAESFARIFYRNAINIG--LPVIMA 107
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Pred. No. 6.7e-15;
9; Mismatches 57;
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Pred. No. !
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                        PID:g15026240;
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A;Experimental source: strain Orsay
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A; Residues: 1-164 < KAW>
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-162 <MTH> A;Residues: 1-162 <MTH> A;Cross-references: GB:AE000901; GB:AE000666; NID:g2622486; PIDN:AAB85864.1; PID:g262249 A;Experimental source: strain Delta H
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                                                                     A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Accession: E69051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --FPI-LECEEAVNDASTGDKLEVDFIEGIIKNVTLNKEYKAOPFPD 143
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||| | ||||||||||||:|: || ::|: :||||:||: | |: |
|--IIVAGENFGCGSSREHAPLAIKAAGVSCVIAKSFARIFYRNAINIG--LPI-LEAPQA 108
                                                                                                                                                                                                                                                                                                                                                                                                          GRAWKYGDNIDTDVIIPARYLN--TSDPKE---LAKHVLEDLDPEFRSK--MKPGD----
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                                                                                                                                                                                                                                                                                          VDRIETGDELEVDESSGEIRNLTKGEVYRANPFPDFIMEIIKAGGLVEWAKR 160
                                                                                                                                                                                                                                                                                                                       WKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGD-AGPVIEAGGIFAYARK 239
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67; Conserv
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38.3%;
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; pred. No. 3.6e-14;
26; Mismatches 62;
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Pred. No. 2.7e-14;
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R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blad; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaso, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaso, A;Teference number: A64300; MUID:96337999; PMID:8688087
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Reterior: F64458
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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F64458
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A; Gene: MTH
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A;Map position: FOR1215638-12161!
C;Keywords: carbon-oxygen lyase;
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A; Residues: 1-170 <B
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                                                                                                                                              54 ----VIVAGENFGCGSSREQAVIAIKYCGIKAVIAKSFARIFYRNAINVGLIPIIANTD
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                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                          VGAWKECKTGDVVTVDLANSVFINHTSGKEYKLK-PIGDAGPVIEAGGIFAYARKTGMIA 244
                                                                                                                                                                      SSRYANITYGGANEGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTD 185
 SX
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                                                                       -EIKDGDIVEIDLDKEEIVITNKNKTIKCETPKGLEREILAAGGLVNYLKKRKLIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:U67568; GB:L77117; NID:g2826383; PIDN:AAB99277.1;
                                                                                                                                                                                                                                                                                                                  19.8%; Score 250.5; DB 2; 35.2%; Pred. No. 1.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.9%;
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Pred. No. 1.
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; jannasc
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C; Paccession: H69469
C; Accession: H69469
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Ki Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J. Gocay

Kirkness, K.A.; Dod 3-isopropylmalate dehydratase, small subunit (leuD-2) homolog - Archaeoglobs C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

small subunit (leuD-2) homolog -

Archaeoglobus

fulgidu

RESULT H69469

13

Sykes,

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3-isopropylmalate dehydratase, small subunit - Deinococcus radiodurans (strain R1) (Speciles: Deinococcus radiodurans (C;Speciles: Deinococcus radiodurans (C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000 C;Accession: F75355 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
hypothetical protein TM0292 - Thermotoga maritima (strain MSB8) C;Species: Thermotoga maritima C;Paccies: Thermotoga maritima C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C;Accession: D73394 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft,
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A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducin A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Accession: H69469
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Cross-references: GB: AE002019;
A: Cross-references: strain R1
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A; Residues: 1-208 <WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A; Reference number: A75250; MUID:20036896; PMID:10567266 A; Accession: F75355
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A;Residues: 1-165 <KLE>
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                                                                                                                                                                                                                                                                                              KTGDVVTVDLANSVFINHTSGKEYKLKPIGD-AGPVIEAGGIFAYAR 238
                                                                                                                                                                                                                                                                                                                                                                                                      VGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGAWKEC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPF---VAPGEESSRYAII 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGDAG-PVIEAGGIFAYARKTGMI 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRAWKFGDDISTDHITPGRYYHLRSNMPELAKHVMEDADPDFMKKFRPGDF----- 55
                                                                                                                                                                                                                                                                                                                                               VAGADFGCGSSREHAVWALRGAGVSAVIAPNFÄRIYYRNSINNGF---LALECEGITELF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHINTDEIIPARHLT-----TDVESELAKYAMED-----YDKDFVRRVQPGD-----II 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -IVAGKNFGMGSSREHAPLALKIAGVSAVIAKSFARIFYRNAINVG--LPVLIADTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.1%; Score 229.5; DB 2; llarity 38.3%; Pred. No. 1.1e-11; Conservative 21; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB:AE000513; NID:g6459547; PIDN:AAF11332.1; PID:g645955
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  Hickey
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Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72394
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-166 <ARN>
A;Residues: 1-166 <ARN>
A;Cross-references: GB:AE001711; GB:AE000512; NID:g4980788; PIDN:AAD35380.1; PID:g498
A;Experimental source: strain MSB8
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C.M.
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Best Local (
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                                                             102 VIELKEY---DEINOGDELEIDLENGVLKNLTTGKEYRFTPI----PKFLLEILKEDGIV 154
                                                                            120 VAPGEESSRYAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVY 179
155 NYLKKHG
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                             241
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; Pred. No. 1.3e-11;
26; Mismatches 60;
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Search completed: March 31, Job time : 46 secs 2003, 09:09:42

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Title:
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                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
              311.5
272.271.1
267.55.252.5.252.5.250.5
250.5.250.5.250.5
250.5.250.5.250.5
1191.5.250.5
1191.5.250.5
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Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
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Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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Nature 390:364-370(1997).
-!- CATALYTIC ACTIVITY: 3-ISOPROPYLMALATE = 2-ISOPROPYLMALEATE +
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUR-2002 (Rel. 41, Last annotation update)
Putative 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)
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0; Mismatches
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Pred. No. 1.6e-15;
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                                                                                                                                                                                                                                                                               Length 161;
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30-MAY-2000
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-isopropylmalate dehydratase small subunit (EC 4.
[Isopropylmalate isomerase) (Alpha-IPM isomerase)
LEUD OR AQ_1398.
Aquifex aeolicus.
Aquifex aeolicus.
Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00694; Aconitase_C; 1.
Leucine biosynthesis; Lyase; Complete proteome.
SEQUENCE 168 AA; 18786 MW; 25A34FE7FFCA09F3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 392:353-358(1998).
-!- CATALYTIC ACTIVITY: 3-ISOPROPYLMALATE = 2-ISOPROPYLMALEATE
H(2)0 (ALSO CATALYSES 2-ISOPROPYLMALEATE + H(2)0 = 3-HYDRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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SUBUNIT: CONSISTS OF TWO DIFFERENT SUBUNITS: LEUC AND LEUD.
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                                                                                                                                                                                                                      FRGRYWKFGDNVDTDQIIPARYLN--TSDPYELAK--
AYAKE - - KLASK
                                                                                                         PLELTDV-GAWKECKTGDVVTVDLANSVFINHTSGKEYKL----KPIGDAGPVIEAGGIF
                                                                                                                                               PEFAKEHKEGDIIVAGKNFGSGSSREHAPIAIKYSGVPVVIAKSFARIFFRNAINIG---
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                                                                      -LPIVEAPEAVDEIEHGDEIEVDLEKGVIKNLRTGKEYQATKFPKELQD---ILKAGGLM
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                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                27;
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Pred. No. 2.1e-15;
27; Mismatches 53;
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15-JUL-1998
15-JUL-1998
15-JUN-2002
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MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

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Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
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Q58673;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)
(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
                                                                                                                                                                                                                                                                                                                     InterPro; IPR000573; Aconitase_C.

Pfam; PF00694; Aconitase_C; 1.

Leucine biosynthesis; Lyase; Complete proteome.

SEQUENCE 168 AA; 18377 MW; A53C2CA883B6CCD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67568; AAB99283.1; TIGR; MJ1277; -.
                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jannaschii.";
Science 273:1058-1073(1996).
-!- CATALYTIC ACTIVITY: 3-ISOPROPYLMALATE = 2
H(2)O (ALSO CATALYSES 2-ISOPROPYLMALEATE
4-METHYL-3-CARBOXYPENTANONE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
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                                                                                                                                                                                                                                                                                     Local
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SUBUNIT: CONSISTS OF TWO DIFFERENT SUBUNITS (POTENTIAL).
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                                                                                                                   CKGISEKVNEGDELEVNLETGEIKNLTTGEVLK----GQKLPEFMMEILEAGGLMPYLKK
                                                                                                                                                                                                                    SIIKGRVWKFGNNVDTDAILPARY--LYYTKPEE---LAQFVMTG-ADPDFPKK-VKPGD
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36, Created)36, Last sequence update)41, Last annotation update)
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Pred. No. 4e-15;
9; Mismatches
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E + H(2)O = 3-HYDROXY-
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Query Match
Best Local
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative 3-isopropylmalate dehydratase small subunit (EC 4.2.1.
(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
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Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
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"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997)
-!- CAMPALYTIC ACTIVITY: 3-ISOPROPYLMALATE = 2-ISOPROPYLMALEATE +
H(2)O (ALSO CATALYSES 2-ISOPROPYLMALEATE + H(2)O = 3-HYDROXY-
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InterPro; IPR000573; Aconitase_C.
Pfam; PF00694; Aconitase_C; 1.
Leucine biosynthesis; Lyase; Complete proteome.
SEQUENCE 170 AA; 18651 MW; BC07146AF7585215 CRC64;
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Methanobacteriaceae;
NCBI_TaxID=187420;
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Smith D.R., Doucette-Stamm L.A.,
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Archaea; Euryarchaeota; Methanobacteria;
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                                                                                                                               Methanobacterium thermoautotrophicum.
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                                                                                                   Archaea; Euryarchaeota;
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SUBUNIT: CONSISTS OF TWO DIFFERENT SUBUNITS (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVGAWKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGD-AGPVIEAGGIFAYARKT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESSRYAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFHGECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGL-PSAAYPTPFVAPGE 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                      Methanothermobacter
                                                                                                   Methanobacteria; Methanobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 266; DB 1;
Pred. No. 5.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                     162
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isomerase) (IPMI).
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A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
A Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
A Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
A Daniels C.J., Mao J.-I., Rice P., Moelling J., Reeve J.N.;
Complete genome sequence of Methanobacterium thermoautotrophicum
AT Complete genome sequence of Methanobacterium thermoautotrophicum
AT deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
J. J. Bacteriol. 179:7135-7155(1997).
J. J. GATALYIC ACTIVITY: 3-1800ROPYLMALEATE + H(2)O = 3-HYDROXY-
H(2)O (ALSO CATALYSES 2-ISOPROPYLMALEATE + H(2)O = 3-HYDROXY-
L. L. STANDANE).
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Best Local
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STRAIN=Delta H;
STRAINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                    058667:
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative 3-isopropylmalate dehydratase small subunit (EC (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000573; Aconitase_C.

pfam; PF00694; Aconitase_C; 1.

Leucine biosynthesis; Lysse; Complete proteome.

SEQUENCE 162 AA; 17956 MW; FF6978208DE0F5B1 CRC64;
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METJA
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanocaldococcaceae; M
                                                                                                                                                                                                                                                                                                                                                                                     Methanococcus jannaschii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFVAPGEESSR 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE000901; AAB85864.1; -.
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                                                                                                                                                                                                                                                                                                                      Methanocaldococcus
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Pred. No. 6.4e-14;
""cmatches 63;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)
(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
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Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B. Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., 2ho
                                                                                                                                                                                                                                                                                                                     LE24_ARCFU 028513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                           STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                        Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00694; Aconitase_C;
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                            NCBI_TaxID=2234;
                                                                                                                                                                            Archaeoglobaceae;
                                                                                                                                                                                                                         AF1761
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SEQUENCE 170 AA; 18665 MW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----EIKDGDIVEIDLDKEEIVITNKNKTIKCETPKGLEREILAAGGLVNYLKKRKLIQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGAWKECKTGDVVTVDLANSVFINHTSGKEYKLK-PIGDAGPVIEAGGIFAYARKTGMIA
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    Glodek A., Zhou L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Putative 3-isopropylmalate dehydratase small subunit (EC (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
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Pfam; PF00694; Aconitase_C; 1.
Leucine biosynthesis; Lyase; Complete proteome.
Leucine biosynthesis; Lyase; Complete proteome.
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Venter
                                                                            MEDLINE-98344137; PubMed-9679194;
Kawatabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Kushida N., Oguchi A.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Aoki K.-I., Yoshizawa T., Kikuchi H.;
Masuchi Y., Shizuya H., Kikuchi H.;
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Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
"Complete sequence and gene organization thermophilic archaebacterium, Pyrococcus DNA Res. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Isopropylmalate PH1724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reducing archaeon Archaeoglobus Nature 390:364-370(1997).
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H(2)O (ALSO CATALYSES 2-ISOPROPYLMALEATE +
4-METHYL-3-CARBOXYPENTANONE).
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30; Mismatches
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No. 1.3e-13;
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                     of the genome of horikoshii OT3.";
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E + H(2)O = 3-HYDROX
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Sykes S.M.,
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01-JUL-1993
01-JUL-1993
15-JUN-2002
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                              lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001)
-!- CATALYTIC ACTIVITY: 3-IS
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-NCDO 2118;
MEDLINE-93015710; PubMed-1400210;
Godon J.-J., Chopin M.-C., Ehrlich S.D.;
"Branched-chain amino acid biosynthesis of the state of the st
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                                                                                                                     Bolotin A., Wincker P., Mauger S., Jaillon Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis (subsp. lactis) (St. Bacteria; Firmicutes; Lactobacillales;
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LEUD OR LL1221.
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Pfam; PF00694; Aconitase_C;
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                                                                                                                                                                                                                       MEDLINE=21235186; PubMed=11337471;
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                                                                                                                                                                                                                                                                                                                                                      Bacteriol.
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H(2)O(ALSO CATALYSES 2-ISOPROPYLMALEATE + H
4-METHYL-3-CARBOXYENTANONE).
PATHWAY: Leucine biosynthesis; second step.
SUBUNIT: CONSISTS OF TWO DIFFERENT SUBUNITS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAWKECKTGDVVTVDLANSVFINHTSGKEYK-----LKPIGD-AGPVIEAGGIFAYARK
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(ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 26, Created)
(Rel. 26, Last sequence update)
(Rel. 41, Last annotation update)
malate dehydratase small subunit (
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3-ISOPROPYLMALATE = 1
ES 2-ISOPROPYLMALEATE
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Pred. No. 7.8e
27; Mismatches
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AEFBDDE1CBCDD266 CRC64;
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lactic
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E + H(2)O = 3-HYDROXY-
2-ISOPROPYLMALEATE
E + H(2)O = 3-HYDROX
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                                                                                                                               Lactococcus
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L outstation -
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Best Local S
Matches 58
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TIGRRAMS; TIGR00171; leuD; 1:
Leucine biosynthesis; Lysse; Complete proteome.
SEQUENCE 191 AA; 21849 MW; C691BC6AAEF4E964 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U92974; AAB81916.1; -.
                                                                                                                 Manna A.C., Das H.K.;
Manna A.C., Das H.K.;
"Characterization and mutagenesis of the leucine biosynthetic
"Characterization and mutagenesis of the rarity of amino
                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
3-isopropylmalate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000573; Aconitase_C.
InterPro; IPR004431; LeuD.
                                                                                                         auxotrophs.";
                                                                                                                                                                MEDLINE=97261869; PubMed=9108283;
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                              Azotobacter vinelandii
                                                                                                                                                                                                                                                                              LEUD.
                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                            P96196;
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SUBUNIT: CONSISTS OF TWO DIFFERENT SUBUNITS: LEUC AND LEUD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4-METHYL-3-CARBOXYPENTANONE).
                           SUBUNIT: CONSISTS OF TWO DIFFERENT SUBUNITS: LEUC AND LEUD.
                                       4-METHYL-3-CARBOXYPENTANONE).

PATHWAY: Leucine biosynthesis; second step.
                                                                  CATALYTIC ACTIVITY: 3-ISOPROPYLMALATE = 2-ISOPROPYLMALEATE + H(2)O (ALSO CATALYSES 2-ISOPROPYLMALEATE + H(2)O = 3-HYDROXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; AE006354; AAK05319.1;
S35135; S35135.
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  SWISS-PROT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                               Genet. 254:207-217(1997).
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entry
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35, Last sequence update)
41, Last annotation update)
dehydratase small subunit (EC
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Pred. No. 7.3e
35; Mismatches
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                                                                                                                                                                                                                                                   subdivision; Pseudomonadaceae;
  Ιt
                                                                                                                                                                                                                                                                                                                                                                            215
                                                                                                                                                                                                                                                                                            isomerase)
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    collaboration
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acid
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Best Local
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P18250;
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InterPro; IPR000573; Aconitase_C.
InterPro; IPR004431; LeuD.
Pfam; PF00694; Aconitase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outsi
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOY-1990 (Rel. 16, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _PHYBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGRO0171; leuD; 1.
Leucine biosynthesis; Lyase.
SEQUENCE 215 AA; 24133 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                 STRAIN-NRRL 1555;
MEDLINE-90356419; PubMed-2388845;
Iturriaga E.A., Diaz-Minguez J.M.,
                                   -i- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
-i- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
                                                                                                                                                                                                                                                                                                                                                                                   Phycomyces.
                                                                                                                                                                                                                                                                                                                                                                                                              Phycomyces
            +
                                                                 Unpublished observations (MA-i- FUNCTION: Catalyzes the
                                                                                            Gibson
                                                                                                                                     Curr. Genet.
                                                                                                                                                  Phycomyces blakesleeanus leul gene.
                                                                                                                                                                             Eslava
                                                                                                                                                                                         MEDLINE=92224296; PubMed=1563047; Iturriaga E.A., Diaz-Minguez J.M.,
                                                                                                                                                                                                                    STRAIN=NRRL 1555;
                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                           Nucleic Acids
                                                                                                                                                                                                                                                            "Nucleotide sequence of the Phycomyces blakesleeanus leul gene.";
Nucleic Acids Res. 18:4612-4612(1990).
                                                                                                                                                                                                                                                                                      Eslava A.P.;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4837;
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         isomerase)
                                                                                                          IDENTIFICATION OF PROBABLE FRAMESHIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 DELFRQCESTEGYRLTVDLAAQT-VTRPDGKALSFEIDP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129
                                                                                                                                                               Heterologous transformation of Mucor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
            H(2)O.
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIDTDQIIPAEHLTLV-----PSKPDEYRKLGSFAFAGLPSAAYP--TPFVAPGEESSR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASYLLARENFGCGSSREHAPWALDEYGFRTVIAPSFADIFFNNSFKNG-LLPIILPEAEV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVDTDQIIPKQFLKSIKRTGFGPNLFDEWRYL-DVGQPGQDCSARPLNTGFVLNLPRYQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -WKECKT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 blakesleeanus
                                                                                                                                                                                                                                                                                                                                                                                                                                         (Alpha-IPM isomerase) (IPMI).
                                                                                                                                                                                                                                                                                                                                                                                                  Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                     21:215-223(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GDVVTVDLANSVFINHTSGK--EYKLKP
                                                                                                                                                                                                                                                                                                                                                                                                  Zygomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.9%;
            2-isopropylmaleate
                                                                                  (MAR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 189;
                                                                                                                                                                                                                                                                                                                                                                                                  Zygomycetes; Mucorales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8E7CC713228005B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                           Benito E.P.,
                                                                                                                                                                                                                                                                                                       Benito E.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          744
                                                                                                                                                                 circinelloides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
              + H(2)0 =
                                                                                                                                                                                                                                                                                                       Alvarez M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                           Alvarez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                     2-isopropylmalate
                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         commercia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on
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isopropylmalate

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LEUZ-SCHP
LEUZ-S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                              LEU2_SCHPO STANDARD; PRT; 758 AA.
014289;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-1sopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate Isomerase) (Alpha-IPM Isomerase) (IPMI).
SPACESO, 03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000573; Aconitase_C.
InterPro; IPR001039; Aconitase_N.
InterPro; IPR004430; LeuC.
InterPro; IPR004431; LeuD.
Pfam; PF00330; aconitase; 1.
Pfam; PF00644; Aconitase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Leucine Divognomer.
-!- SUBUNIT: MONOMER.
-!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
-:- SIMILARITY: Ref.1 and Ref.2 sequences differ from that shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00694; Aconitase_C; 1. PRINTS; PR00415; ACONITASE. PR000051; ACONITASE_N; 1. TIGRFAMS; TIGR00170; leuC; 1. TIGRFAMS; TIGR00171; leuD; 1.
MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M.A., Sgouros J., Peat N., Hayles J., Baker
                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00450; ACONITASE_1; 1. PROSITE; PS01244; ACONITASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S10998; S10998
PIR; S26864; S26864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X53090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                      Schizosaccharomyces.
                                                                                                                                                                                                            Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 GLGSALFYGLRYDPATGAEKPDFVLNQPAYRSSK-ILVCTGPNFGCGSSREHAPWAFNDF 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 GARAIVAEGYARIFFRNSVATGEVYPLELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 CRRAGSIVPAAAAAAAGSSSPSSAVFHGECFVVG-DNIDTDQIIPAEHLTLVPSKPDEYR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLGSEAFAGL---PSAAYPTP-FV--APGEESSRYAIIVGGANFGCGSSREHAPVALGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPPAGS--PVNKGAPVASAMPAFTTLKGVAAPLAISNVDTDMIIPKQFL----KTIKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIRCIIATSFADIFFNNCFKNG-MLPIILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biosynthesis; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAA37257.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80833 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.5%;
                                                                                                                                                                                                            Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Iron-sulfur; 4Fe-4S.
IRON-SULFUR (4FE-4S) (BY S
IRON-SULFUR (4FE-4S) (BY S
IRON-SULFUR (4FE-4S) (BY S
W; .9E5A930891D3745C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 184; DB 1;
Pred. No. 1.4e-07;
m M.A., Lyne M.,
Baker S., Basham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         639
  Lyne
m D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
     R., Ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
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                           Stewart A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
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578

156

ARAIVAEGYARIFFRNSVATGEV-YPLELTDVGAWKECKTGDV-VTVDLANSVFINHTSG

AF----YEIRYDADGKEIPDFVLNREPYRHATVLVAHDNFGCGSSREHAPWALNDFG

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δÃ
                                                В
                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA James K., Jones M., Eather S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA RA Kitherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Kyelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vonstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Weltjens I., Vonstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Cerrutti I., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti I., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti I., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti I., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti I., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti I., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Challes S., Lehrach H., Ra Challes S., Valles S., Lehrach M., Stayer S., Lehrach M., Stayer S., Lehrach M., Stayer S., Lehrach M.
                                                                                                                                       Query Match
Best Local S
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR004431; LeuD.
Pfam; PF00330; aconitase; 1.
Pfam; PF00694; Aconitase_C; 1.
PRINTS; PR00415; ACONITASE.
PRODOM; PD000511; Aconitase_N; 1.
TIGRFAMS; TIGR00170; LeuC; 1.
TIGRFAMS; TIGR00171; leuD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z99262; CAB16402.1; -.
InterPro; IPR000573; Aconitase_C.
InterPro; IPR001030; Aconitase_N.
InterPro; IPR004430; LeuC.
InterPro; IPR004431; LeuD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                  PROSITE; PS00450; ACONITASE_1; 1.
PROSITE; PS01244; ACONITASE_2; 1.
Leucine biosynthesis; Lyase; Iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                SEQUENCE
    106
                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isopropylmalate.
PATHWAY: Leucine biosynthesis; second step.
PATHWAY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H(2)0. CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                         AAAAAGSSSPSSAVFHGECFVVG-----DNIDTDQIIPAEHLTLVPSKPDEYRKLGSF
                                                  ATNVAGSVSSGSAGIPKFTVVEGIAAPLPMANVDTDKIIPKQFL----KTIKKTGLGQF
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                758 AA;
                                                                                                                                                                                                                                                        420
423
                                                                                                                                         Conservative
                                                                                                                                                                                                                                420
423
82782
                                                                                                                                    14.5%; Score 183.5; DB 1
32.1%; Pred. No. 1.6e-07;
cive 19; Mismatches 77
                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                           ;; Iron-sulfur; 4Fe-4S.
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
    --AIIVGGANFGCGSSREHAPVALGAAG
                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                   (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                         Indels
                                                                                                                                                                                Length 758;
                                                                                                                                         31;
                                                                                                                                         Gaps
       155
                                                  577
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VKFDVEP KEYKLKP

RHINI

EU2_RHINI

STANDARD;

750

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631

IRVIIAPSFADIFFNNCFKNGMLPIPTPIEQVNDMMKAAENQVKFSVDLVNQTITYGDKQ 690

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EESULU PAR RESULU PAR 
                        Ş
                                                                                            Query Match
Best Local
                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
3-isopropylmalate
                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00330; aconitase; 1. Pfam; PF00694; Aconitase_C; 1. PRINTS; PR00415; ACONITASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                               ProDom; PD000511; Aconitase_N; 1.
TIGRFAMs; TIGR00170; leuC; 1.
TIGRFAMs; TIGR00171; leuD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
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                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             somerase) (Alpha-IPM
                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Leucine biosynthesis; second step.
SUBUNIT: MONOMER (By similarity).
SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isopropylmalate.
PAAAAAAAGSSSPSSAV<del>IHG</del>ECFVVG-DNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D63833;
                                                                                            Similarity
                                                                                                                                                                                                                                                             biosynthesis;
                                                                                                                                                                                                                                                                                 PS00450; ACONITASE_1; PS01244; ACONITASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000573; Aconitase_C. IPR001030; Aconitase_N. IPR004430; LeuC. IPR004431; LeuD.
                                                                                                                                                              413
416
750
                                                                      Conservative
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                                                                                                                                                                   AA;
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1. 35, Last sequence update)
1. 41, Last annotation update)
te dehydratase (EC 4.2.1.33) (If
ha-IPM isomerase) (IPMI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
                                                                                                                                                                   $1308
81308
                                                                                            34.5%;
                                                                                                                                                                                                                                                        Lyase;
                                                                                                                                                                MW;
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                                                                                                                                                         Iron-sulfur; 4Fe-4S.
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
; 7D7BE28304E26AB3 CRC64;
                                                                                               Pred.
                                                                                                                  Score
                                                                      Mismatches
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RX KEDLINE-98044033; PubMed=9384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniell R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniell R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniell R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizri B., Foulger D.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Mauel C., Medique C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogivara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Persecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Yoshida K., Yashancto K., Yata K.,
Tanka T., Tarkhashi H., Takhasa H., Danchin A.,
The Complete genome sequence of the Gram-positive bacterium Bacillus
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)
(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
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Bacteria; Firmicutes;
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                                                                                 Nature 390:249-256(1997).
-!- CATALYTIC ACTIVITY: 3-ISOPROPYLMALATE = 2-ISOPROPYLMALEATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiology 142:3067-3078(1996).
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CATALYTIC ACTIVITY: 3-ISOPROPYLMALATE = 2-I
H(2)O (ALSO CATALYSES 2-ISOPROPYLMALEATE +
4-METHYL-3-CARBOXYPENTANONE).
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Best Local Similarity
Matches 53; Conserv
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EMBL; Z99118; CAB14785.1; -.
Subtilist; BG11950; leub.
InterPro; IPR000573; Aconitase_C.
InterPro; IPR004431; Leub.
Pfam; PF00694; Aconitase_C; 1.
TIGRFAMs; TIGR00171; leub; 1.
Leucine biosynthesis; Lyase; Complete proteome.
SEQUENCE 199 AA; 23022 MW; 99ADFE1ZAOD5D9D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Leucine biosynthesis; second step.
-!- SUBUNITS: CONSISTS OF TWO DIFFERENT SUBUNITS: LEUC AND LEUD.

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124 DNWKQL-VGQYENQSLQMTVDLENQL-IHDSEGNQ 156
                                                                         187 GAWKECKTGDV------VTVDLANSVFINHTSGKE 215
                                                                                                                                                                             77 NIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFVAPGEESSRY------ 129
                                                                                                                                                        18 NVDTDQIIPKQFL----KRIERTGYGRFAF-----FDWRYDANGEPNPEFELNQPVY 65
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sp_virus:*
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Q92W85
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Q91YT7
Q91YT7
Q91YE1
Q8U2A0
Q8U2A0
Q8TX94
Q8TX94
Q8TDK1
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Q92w85
Q91yt7
Q91yt8
Q91ye8
Q812a0
Q812a0
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0 deinococcus
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8 thermotoga
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5 arabidopsis
7 arabidopsis
4 arabidopsis
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thermoanaer
methanosarc
sulfolobus
                                                                                                      pyrococcus
clostridium
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	3	30	29	28	27	26	25	24	23	22	21	20	19	18	17
158.5	159	159.5	161.5	163	167.5	168	168.5	169	169.5	170	170	171.5	172.5	174.5	174.5	176.5	178	179.5	182.5	184	188	189	192	202	206.5	210	212	222
•				12.9	13.2	13.3	13.3	13.3	13.4	13.4	13.4	13.5	13.6	13.8	13.8	13.9		14.2	14.4	14.5	14.8	14.9	15.2	16.0	16.3	16.6	16.7	17.5
211	190	182	177	201	216	200	201	213	193	213	201	202	641	194	193	201	196	711	216	212	215	202	659	163	163	164	168	168
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Q8YCW7	Q99SJ2	Q938C8	Q9RTY5	Q9CJN8	Q8UBR0	Q9KP80	Q98E51	Q9JU81	Q92A25	Q9JZI6	Q8RP98	Q9ABN1	Q8RCF8	Q9K8F1	Q8Y5R6	Q92LA1	Q9AIM2	Q9P3Y5	Q8XXX4	Q9HZA4	Q9PAX1	COXABO 3	067656	Q9ZND9	Q9V1I9	Q8U0B9		Q974Q9
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ALIGNMENTS

PRELIMINARY;

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AC Q949
AC Q949
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DT 01-D
DT 01-D
DT 01-J
DC HYPO
GN C740
OS CTYZ
OC Ehrh
OX NCBI
RN [1]
RP SEQU
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RA Maye
RA Haas
RA Haas
RA Beva
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RT Geno
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RT Geno
DR EMBLI
RM HYPO
SQU SEQU
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                                                                                         Query Match
Best Local Similarity
Matches 197; Conserv
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EMBL; AJ307662; CAC39061.1; -.
InterPro; IPR000573; Aconitase_C.
Pfam; PF00694; Aconitase_C; 1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 257 AA; 26443 MW; 7EC420ECE735FB66 CRC64;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-21329048; PubMed=11435398;

Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T.,

Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T.,

Hasse D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W.,

Bevan M., Bancroft I.;

"Conservation of microstructure bewtween a sequenced region of the
genome of rice and multiple segments of the genome of Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.4 kDa protein.
C740ERIPDM.
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Q949D1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                      thaliana.";
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                          1 MAAALSGTAVSTA-----ALLAPIRAPTSAFIRRSQLTCHRLHSLKC---RRAGSIVPA 51
MAAAAAAPALSLAEAAPVTAVLAPCPTPSRTFRRRSWVAAICRPALKCHHSRPLTAVAAA
                                                                                78.2%; Score 990.5; DB 10; Length 257; ilarity 76.7%; Pred. No. 4.6e-76; Conservative 18; Mismatches 33; Indels 9;
                                                                                   Gaps
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SEQUENCE FROM N.A.

RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kariln-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M
Shinn P., Southwick A., Tracy S.E., Shinozaki K.
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
3-isopropylmalate dehydratase, small subunit (Putative)
3-isopropylmalate dehydratase small subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. COLUMBIA;

MEDLINE-20083487; PubMed-10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,

Cronin L.A., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Nierman W.C., White O., Eisen J.A.,
                                                                                                                                                                                                                Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida Jones T., Kamiya A., Karlin Neumann G., Kawai J., Kim C., Koesema Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A., "Full Length cDNA of gene F14B2.3/At2g43090 (GI:3763918)."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M.D., Carrera A.J., Creasy T.H., GOOdman H.M., SOUNCELVILLE
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AT2G43090 OR F14B2.3/AT2G43090.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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InterPro; Lr.
PF00694; Acu.
251 AA;
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                                                                                                                                                                                                                                                                                                                                                                                    3-isopropylmalate dehydratase small subunit).
F17J16 40 OR AT3658990.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EMBL; AC004450; AAC64298.1; -.
EMBL; AY035158; AAK59662.1; -.
EMBL; AY063029; AAL34203.1; -.
EMBL; AC006224; AAM15163.1; -.
InterPro; IPR000573; Aconitase_C.
Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M.,
                                                                                                                                                                                                                                                 D'Angelo M., Vezzi A., Rudd S., Lemcke K., Ma Submitted (APR-2000) t
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Pred.
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No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Embryophyta;
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                                                                                                                                                                   databases
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eudicots; Rosidae;
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RRA A A CORRESPONDE CONTRA CON

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"Full Length cDNA of gene At3g58990
Submitted (DEC-2001) to the EMBL/Ge
EMBL; AL163527; CAB86927.1;
EMBL; AV065366; AAL38807.1;
InterPro. IPR000573; Aconitase_C.
Pfem; PF00694; Aconitase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9ZW84 PRELIMINARY; PRT; 256 AA.
Q9ZW84;
Q9ZW84;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-SUN-2002 (TrEMBLrel. 20, Last annotation update)
Q1-SUN-2002 (TrEMBLrel. 21, Last annot
                                                                                                                                                                                                                                                                                                MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O.; Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AT2G43100.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta;

Spermatophyta; Magnoliophyta; endicotyle
eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Narusaka Narusaka Narusaka
Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.
                                                                                                                                                                                                                                                       Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                              FROM N.
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Southwick
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AA; 27208 M
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Shinozaki 1
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Pred. No. 2.6e
29; Mismatches
                                                                                                                                                             EMBL/GenBank/DDBJ
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edons; core e
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.6e-47;
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A Carrera A.J., Creasy T.H., Buell C.R., Town C.D., N.
Fraser C.M., Venter J.C.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ datable EMBL; AC004450; AAC64299.1;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ datable EMBL; AV063028; AAL361219.1;
EMBL; AY06394; AAL31219.1;
RINTERPROJECT 1000573; ACONITASE_C.
RINTERPROJECT 1000573; ACONITASE_C.
REGUENCE 256 AA; 27043 MW; 56845DC3F4F90A65 CRC
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Shinn P., Southwick F
Theologis A.;
"Full Length cDNA of
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Ol-JUN-2002 (TrEMBLrel. 21,
Ol-JUN-2002 (TrEMBLrel. 21,
Ol-JUN-2002 (TrEMBLrel. 21,
Ol-JUN-2002 (TremBlrel. 21,
Putative 3-isopropylmalate
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                                                                                                           Pyrococcus furiosus.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                           Q8U2A0
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                                                                                                                                                                             PF0939.
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Shinozaki
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EMBL/GenBank/DDBJ databa
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No. 2.
                                                                                                                 Thermococcales;
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.8e-45;
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C.M., Benito
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                                                                                                                 Thermococcaceae;
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Matches 68
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Best Local
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         097EE1 PRELIMINARY; PRT; 163 AA.
097EE1; O1-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
3-isopropylmalate dehydratase, small subunit.
CAC3172.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL; AE007812; AAK81109.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=ATCC 824 /
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                                                                                                                                                                                                                                                                     HGECFVVGDNIDTDQIIPAEHL-TLVPSK--------PDEYRKLGSFAFAGLPSAAYP 116
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                                                   EVYPLELTDVGAWKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGD 223
                                                                                                                                       TPFVAPGEESSRYAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATG 176
                                                                                                                                                                                                                              NGDVLKYGDNIDTDVIIPARYLNTSVPEELAKHCMEDLDVDFLKKLKT---
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FPI-LECEEAVNDASTGDKLEVDFIEGIIKNVTLNKEYKAQPFPD 143
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 AA;
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                                                                                                               IVVGGRNFGCGSSREHAPICIKAAGVSCVIAKSFARIFYRNSINIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18025 MW;
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                                                                                                                                                                                                                                                                                                                                          20.5%; score 260; DI 38.3%; Pred. No. 1.90 cive 22; Mismatches
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1.9e-14;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
3-isopropylmalate dehydratase, small subunit (LEUD-1).
LEUD-1 OR PAB0892.
                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-AV19 / DSM 6324 / JCM 9639;

MEDLINE-2197647; pubMed=11930014;

Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

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Malykh A.G., Koonin e. V., Kozyavkin S.A.;

Malykh Complete genome of hyperthermophile Methanopyrus kandleri AV19

and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

EMBL; AE010370; AAM01995.1; -.
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01-JUN-2002 (TIEMBLIEL 21, Last sequence update)
01-JUN-2002 (TIEMBLIEL 21, Last annotation update)
3-isopropylmalate dehydratase small subunit.
LEUD_1 OR MK0781
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Pfam; PF00694; Aconitase_C; 1.
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submitted (JUL-1999) to the EMBL/GenBank/DDBJ
EMBL; AJ248287; CAB50256.1; -.
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Archaea; Euryarchaeota;
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Archaea; Euryarchaeota;
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                                                                                                SEQUENCE 170 AA;
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66; Conser
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                                                                                                AA;
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                                                                                                     18686
                        20.1%;
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                                                                                                     MW;
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                     Score 254.5;
Pred. No. 6e-
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RESULT 10
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ID Q8TU7
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01-JUN-2002 (TremBLrel. 2
01-JUN-2002 (TremBLrel. 2
01-JUN-2002 (TremBLrel. 2
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"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
EMBL; AE012976; AAM23335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
3-isopropyimalate dehydratase small subunit.
                                                    Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
                                                                                             3-isopropylmalate dehydratase. LEUD OR MA0202.
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STRAIN-MB4T / JCM11007;
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                                       NCBI_TaxID=2214;
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RESULT 11
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Matches 62
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RG Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RG Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Grahame D.E., Grahame D.A., Guss A.M.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Leigh J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Springer T.A., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
The genome of Methanosarcina acetivorans reveals extensive metabolic
Cenome Res. 12:532-542(2002).
                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                  Pfam;
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Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002)
EMBL; AE009851; AAL63866.1; -
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Miller J.H.;
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SEQUENCE FROM N.A.
STORBATN-IM2 / ATCC 51768 / DSM 7523;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
3-isopropylmalate dehydratase small subunit (leuD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8ZW36;
01-mAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8ZW36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 162 AA;
                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                          Complete proteome
                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000573; Aconitase_C.
Pfam; PF00694; Aconitase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAE1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE010678; AAM03655.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the hyperthermophilic crenarchaeon
   129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107
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nes 62; Conserv
                                                         u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRAWKFGDDVDTDAVIPGRY--LIFNTPGE---LAKYTFEGVRPDFA-----KKVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGL-PSAAYPTPFVAPGEESS 127
   YAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGA 188
                                                         GRALVYGDKIDTDVIIPAKYLVYT-----DPALLGQHAMEPL-DPEFP-----KKAK 50
                                                                                                            GECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFVAPGEESSR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- DRIDDGDELEVDLSTGDIQNITKGETYQATPLPDFVREIVDEGGLIEYARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AWKECKTGDVVTVDLANSVFINHTSGKEYKLKPIGD-AGPVIEAGGIFAYARK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENDIVVAGSNFGCGSSREHAPLALKGSKVSCVIAKSFARIFFRNAINIG-VPVLECPNT-
                                                                                                                                                                  1 Similarity
63; Conser
                                                                                                                                                                                                                                                                                  161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 AA;
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17825 MW;
                                                                                                                                                                                                                                                                                  17175 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.9%;
                                                                                                                                                                                             18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                  29;
                                                                                                                                                                  Score 231; DE
Pred. No. 5.5e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 252; DB 17;
Pred. No. 9.1e-14;
1; Mismatches 60
                                                                                                                                                                                                                                                                                  440B9AA6AF3F45A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2D609D9BA176A228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161
                                                                                                                                                            DB 17;
5.5e-12;
mes 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AΑ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 162;
                                                                                                                                                                                                                        Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrobaculum
                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                  Gaps
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REPARATION OF THE PROPERTY OF 
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RESULT 13
QASTRF
ID QASTRF
AC QASTRF
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O1-JU
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GN LEUC
OS Metha
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OC Metha
OC NCBL
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
3-isopropylmalate dehydratase, small subunit.
                                                                                                                                                                               Q8TRF7;
Q8TRF7;
01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deinococcus radiodurans.
Bacteria: Thermus/Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RTIO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9RTI0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE002019; AAF11332.1;
TIGR; DR1784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deinococcaceae;
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000573; Aconitase_C.
Pfam; PF00694; Aconitase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                        Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococo
Methanosarcinaceae; Methanosarcina.
NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the radioresistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20036896; PubMed=10567266;
                                                                                                                               3-isopropylmalate dehydratase.
LEUC OR MA1223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REKYKDGDEVELDVEGGIVRNITTGEVIVGKPLRGLPLEILKAGGLLNYLKNS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGGANFCCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGAWKEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPF---VAPGEESSRYAII 132
                                                                                                                                                                                                                                                                                                                                                                                                                        QDGEEAELDLKGGT IRNPRTGKELSFVPVPQFALDVQKAGGWLEYMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTGDVVTVDLANSVFINHTSGKEYKLKPIGD-AGPVIEAGGIFAYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAGADEGCGSSREHAVWALRGAGVSAVIAPNEARIYYRNSINNGF---LALECEGITELF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22652 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.1%;
                                                                                 Methanococci;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                Last
                                                                                                                                                                                       Last annotation
                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 229.5; DB Pred. No. 1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F26C4BB27FBED1E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208
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                                                                                   Methanosarcinales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
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ij

Matches

64; Conser

26;

Mismatches

Indels

37;

7;

Pred. No.

.1e-11;

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Qy
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STRAINCEAN ATCC 35395 / DSM 2834;

RX MEDLINE=21929760; PubMed=11932318;

RX MEDLINE=21929760; PubMed=11932318;

RX AFILTHUGH W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA FILTHUGH W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA Linton L., McEwan P., McKernan N., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., McKernan K., Talamas J., Grahame D.A., Guss A.M.,

RA Linton L., McEwan P., McKernan K., Graham D.E., Grahame D.A., Guss A.M.,

RA Linton L., McEwan R., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Hedderich R., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic

"The genome Res. 12:532-542(2002).

REL Genome Res. 12:532-542(2002).

REL Genome Res. 12:532-542(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
Query Match
Best Local
                                                                                                                                                                  STRAIN-MSB8 / DSM 3109;
MEDILINE-99287316; pubMed-10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
McDonald L., Utterback T.R., Malek J.A., Flinher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Teyidence for lateral gene transfer between Archaea and Bacteria fragenome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-C2A / ATCC
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9WYC8;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9WYC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-isopropylmalate
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermotoga
                                                                                                                                   TIGR; TM0292;
                                                                                            Pfam; PF00694; Aconitase_C;
                                                                                                                 InterPro; IPR000573; Aconitase_C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRVWKFGDDINTDAIIPGKYL-----RTRDMQIFGTHAMEGIDPEF--TKKAKPGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFVAPGEESSR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --ECQEGDEIKVDLFKGEVLVPEKGIFKGNKLPDF--LLDILNDGGLVAHRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --IIVAGTNFGCGSSREQAPLALKHSGIACIVAKSFARIFFRNAINIG--LPLMEADV--
                                                                                                                                                   AE001711; AAD35380.1;
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                                                                          proteome.
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9 (TrEMBLrel. 12,
1 (TrEMBLrel. 19,
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                                                          A,
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37.0%;
                                                          18734 MW;
   18.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermotogales;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 227.5; DB 1
Pred. No. 1.1e-11;
                       Score 227.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7D46606C68589AC0 CRC64;
                                                            D8ACF340205111A4 CRC64;
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                         DB 16;
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                         Length 166;
                                                                                                                                                                                                                 Bacteria from
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20 STRAIN-C2A / ATCC 35395 / DSM 2834;

22 STRAIN-C2A / ATCC 35395 / DSM 2834;

23 MEDLINE-21929760; PubMed-11932238;

24 Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

25 FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

26 Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

27 ALInton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

28 Alimer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

29 ALImmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

20 ALImmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

20 ALImmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

21 ALIMER A., J. W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

22 ALIMER T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

23 ARA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

24 ARA Springer T.A., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

25 ARA Metcalf W.W., Birren B.;

26 The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 62; Conserv
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OBTJM9:
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
3-isopropylmalate dehydratase.
LEUD OR MA3751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and physiological diversity.";
Genome Res. 12:532-542(2002).
EMBL; AE011086; AAM07104.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 166 AA;
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NCBI_TaxID=2214;
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Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
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156 HRKK 159
                                                                      236 YARK 239
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                                                                                                                                                --ECQEGDEIEVDLLKGEVRVPGKGVF----
                                                                                                                                                                                                              WKECKTGDVVTVDL-----ANSVFINHTSGKEYKLKPIGDAGP-----VIEAGGIFA 235
                                                                                                                                                                                                                                                                                         YAIIVGGANFGCGSSREHAPVALGAAGARAIVAEGYARIFFRNSVATGEVYPLELTDVGA 188
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--IIVAGENFGCGSSREQAPLAIKHAGIACVVAKSFARIFFRNAINVG--LPLMEADI-- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GECFVVGDNIDTDQIIPAEHLTLVPSKPDEYRKLGSFAFAGLPSAAYPTPFVAPGEESSR 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GRVWKFGDDIDTDVIIPGKYL-----RTKDMQIFAAHAMEGI--APEFTKKAKPGD---- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.8%; Score 225.5; DB 17; Length 166; ilarity 33.7%; Pred. No. 1.7e-11; Conservative 28; Mismatches 49; Indels 45;
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                                                                                                                                                -----VGNKLPDFLLDILTDGGLVS
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Search completed: March 31, 2003, 09:08:53 Job time: 37 secs

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